

SEARCH REQUEST FORM

Scientific and Technical Information Center

Access DB#

52619

Requester's Full Name: _____ Examiner #: _____ Date: _____
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 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher _____	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone # _____	AA Sequence (#) <u>1</u>	Dialog _____
Searcher Location _____	Structure (#) _____	Questel/Orbi: _____
Date Searcher Picked Up <u>10/16/07</u>	Bibliographic _____	Dr Link _____
Date Completed <u>10/16/07</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems <u>EV</u>
Clerical Prep Time _____	Patent Family _____	WWW/Internet _____
Online Time _____	Other _____	Other (specify) _____

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 13, 2001, 01:44:58 ; Search time 54.72 Seconds
(without alignments)
517.853 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116

Sequence: 1 MIFPMKQSGTQRDLMNIFKL.....WLARRKKGKSKRSMDNPY 372

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

1: PIR68:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2090	98.8	385	1 A34015	L-selectin precurs
2	1992	94.1	372	2 JC5377	L-selectin precurs
3	1796	84.9	376	2 JC4892	L-selectin precurs
4	1682	79.5	370	2 S22124	L-selectin precurs
5	1653	78.1	372	2 S23936	L-selectin precurs
6	1652	78.1	323	1 S08702	L-selectin precurs
7	1651	78.0	372	1 A33375	L-selectin precurs
8	905	42.8	830	2 A30359	P-selectin precurs
9	902.5	42.7	768	2 A42755	P-selectin precurs
10	894.5	42.3	646	2 JN0473	P-selectin precurs
11	885	41.8	768	2 I53821	P-selectin - rat
12	862	40.7	610	2 A35046	E-selectin - rat
13	861	40.7	551	2 I46709	endothelial leukoc
14	857	40.5	612	2 B42755	E-selectin - bovin
15	849.5	40.1	485	2 S36772	E-selectin - bovin
16	815.5	38.5	482	2 JCS092	E-selectin - pig
17	236	11.2	868	2 T20239	hypothetical prote
18	212.5	10.0	1019	2 A38738	coagulation factor
19	199.5	9.4	449	1 NBH0HS	complement factor
20	199.5	9.4	1231	1 NBH0HS	complement factor
21	175.5	8.3	2014	2 I36936	complement C3b/C4b
22	172	8.1	2	173012	complement C3b/C4b
23	171.5	8.1	597	1 S53711	C4b alpha chain p
24	170	8.0	404	2 A46274	HIV gp120-binding
25	168	7.9	2132	1 A55182	aggreccan precursor
26	167	7.9	321	1 LNBUER	IgE Fc receptor II
27	167	7.9	1234	1 NBMSH	complement factor
28	166.5	7.9	558	2 S57953	C4b protein alpha
29	166	7.8	1456	1 A36563	mannose receptor p

30	165.5	7.8	560	2 T16833	hypothetical prote
31	165.5	7.8	1479	2 T42710	mannose receptor,
32	165	7.8	311	1 LNBU2A	asialoglycoprotein
33	164.5	7.8	482	2 A34924	complement C3b/C4b
34	163	7.7	669	2 S65551	factor H - bovine
35	163	7.7	2124	2 A28452	proteoglycan core
36	162.5	7.7	345	1 NBBO	apolipoprotein H p
37	162	7.7	304	2 JX0209	lectin, galactose/
38	162	7.7	1574	2 T13954	MEGF6 protein - ra
39	161	7.6	469	1 NBMS04	C4b-binding protel
40	160.5	7.6	1455	1 A48925	mannose receptor p
41	160	7.6	1091	1 PL0009	complement C3d/Eps
42	160	7.6	2415	1 A39086	aggreccan precursor
43	159	7.5	1360	2 A39808	proteoglycan core
44	159	7.5	2327	2 T42630	aggreccan - bovine
45	157	7.4	331	1 LNMSER	IgE Fc receptor, 1

ALIGNMENTS

RESULT 1
A34015
L-selectin precursor, long splice form - human
N:Alternate names: CD62L; leucocyte cell adhesion molecule-1 (LECAM-1, LAM-1); leukoc
ral lymph node homing receptor Leu-8
C/Spectes: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C/Accession: I55333; S06798; J10104; A34015; A33912
R/Ord, D.C.: Ernst, T.J.; Zhou, L.J.; Rambaldi, A.; Spertlin, O.; Griffin, J.; Tedder
J. Biol. Chem. 265, 7760-7767, 1990
A:Title: Structure of the gene encoding the human leukocyte adhesion molecule-1 (TL1,
A:Reference number: I55333; MUID:90243637
A:Accession: I55333
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 14-385 <ORF>
A:Cross-references: GB:M32414; NID:g187259; PIDN:AA60700.1; PID:g386660
R/Camerini, D.; James, S.P.; Stamenkovic, I.; Seed, B.
Nature 342, 78-82, 1989
A:Title: Leu-8/TL1 is the human equivalent of the Mel-14 lymph node homing receptor.
A:Reference number: S06798; MUID:90044046
A:Accession: S06798
A:Molecule type: mRNA
A:Residues: 1-225, 'S', 227-385 <CAM>
A:Cross-references: EMBL:X17519; NID:g34344; PIDN:CA843536.1; PID:g4902829
A>Note: this translation is not annotated in GenBank entry HSL8U8, release 111.0
R/Tedder, T.F.; Isaacs, C.M.; Ernst, T.J.; Demetri, G.D.; Adler, D.A.; Distche, C.M.
J. Exp. Med. 170, 123-133, 1989
A:Title: Isolation and chromosomal localization of cDNAs encoding a novel human lymph
oteins.
A:Reference number: J10104; MUID:89310350
A:Accession: J10104
A:Molecule type: mRNA
A:Residues: 1-230, 'N', 232, 'N', 234-254, 'E', 256-385 <TEPD>
A:Cross-references: GB:X16150; NID:g34428; PIDN:CA843275.1; PID:g34429
A>Note: the translated sequence in GenBank entry HSLVAM1, release 111.0, differs from
J. Bowen, B.R.; Nguyen, T.; Lasky, L.A.
J. Cell Biol. 109, 421-427, 1989
A:Title: Characterization of a human homologue of the murine peripheral lymph node ho
A:Reference number: A34015; MUID:89308861
A:Accession: A34015
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 14-49, 'Y', 51-190, 'N', 192-205, 'L', 207-226, 'F', 228-385 <BOW>
A:Cross-references: GB:X16070; NID:g38092; PIDN:CA843203.1; PID:g38093
R/Siegelman, M.H.; Welsman, I.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 5562-5566, 1989
A:Title: Human homologue of mouse lymph node homing receptor: evolutionary conservati
A:Reference number: A33912; MUID:89315837
A:Accession: A33912
A>Status: preliminary
A:Molecule type: mRNA

A:Residues: 14-205, 'L', 207-385 <SIE>
 A:Cross-references: GB:M25280; NID:g187182; PIDN:AAC63053.1; PID:g307134
 C:Comment: For an alternative splice form, see PIR:S05702.
 C:Genetics:
 A:Gene: GDB:SELL; GDB:LNHR; LSEL; LAM1; LYAM1; LAM-1
 A:Cross-references: GDB:120157; GDB:118834; OMIM:153240
 A:Map position: 1922-1923
 A:Introns: 14/3; 42/1; 171/1; 207/1; 269/1; 331/1; 374/1; 380/2
 C:Function:
 A:Description: binds with low affinity to oligosaccharides like heparan sulfate and sialyl
 ment of leucocytes to areas of inflammation, and with CD162 mediates neutrophil-neutrophil
 C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology;
 C:Keywords: alternative splicing; cell adhesion; duplication; glycoprotein; inflammation
 F:1-51/Domain: signal sequence #status predicted <Sig>
 F:4-168/Domain: C-type lectin homology <LCH>
 F:52-385/Product: L-selectin #status predicted <MAT>
 F:52-385/Domain: extracellular #status predicted <EXT>
 F:173-204/Domain: EGF homology <EGF>
 F:210-267/Domain: complement factor H repeat homology <FHI>
 F:212-329/Domain: complement factor H repeat homology <FHI2>
 F:344-368/Domain: transmembrane #status predicted <TM>
 F:369-385/Domain: intracellular #status predicted <INT>
 F:73,117,190,245,259/Binding site: carbonylate (Asn) (covalent) #status predicted
 F:377,380/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 98.8%; Score 2090; DB 1; Length 385;
 Best local Similarity 98.9%; Pred. No. 4,8e-148;
 Matches 368; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIFPMKQSTORDLWNIIFKLMGWTMLCDPLAHGTYCWTYHSEKPMNQARRCRDN 60
 DB 14 MIFPMKQSTORDLWNIIFKLMGWTMLCDPLAHGTYCWTYHSEKPMNQARRCRDN 73
 QY 61 YTDVLAIONKAELEYEKLTPESRSYTWGIRKIGIMTWGNTKSLTEAEWNGGEPRN 120
 DB 74 YTDVLAIONKAELEYEKLTPESRSYTWGIRKIGIMTWGNTKSLTEAEWNGGEPRN 133
 QY 121 NKNKEDCEYIYIKRNKDGKWNDDACHKRLKALCYTASCPWMSGHGECEIINNTTC 180
 DB 134 NKNKEDCEYIYIKRNKDGKWNDDACHKRLKALCYTASCPWMSGHGECEIINNTTC 193
 QY 181 NCDVGYGQCQVLVIOCEPLEPELGTMDCTHPFNGFSSSCAFSCSEGTNLGIEETT 240
 DB 194 NCDVGYGQCQVLVIOCEPLEPELGTMDCTHPFNGFSSSCAFSCSEGTNLGIEETT 253
 QY 241 CGPFGMWSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSPSACFTICSEGTNLGIEETT 300
 DB 254 CGPFGMWSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSPSACFTICSEGTNLGIEETT 313
 QY 301 TICSSGIMSNPSPICQKLDKSFMSIKEDGYNPLFIPAVVMTAFSGLAFTIIMLARLKK 360
 DB 314 TICSSGIMSNPSPICQKLDKSFMSIKEDGYNPLFIPAVVMTAFSGLAFTIIMLARLKK 373
 QY 361 GKSKRSMDPY 372
 DB 374 GKSKRSMDPY 385

RESULT 2
 JC5377
 L-selectin precursor - hamadryas baboon
 C:Species: Papio hamadryas (hamadryas baboon)
 C:Accession: JC5377; PC4315
 C:Date: 02-Jun-1997 #sequence_revision 12-Sep-1997 #text_change 21-Jan-2000
 R:Tsushima, N.; Fu, H.; Berg, E.L.
 A:Title: PCR cloning of the cDNA encoding baboon L-selectin.
 A:Reference number: JC5377; MUID:97128794
 A:Accession: JC5377
 A:Molecule type: mRNA
 A:Residues: 1-372 <TSU1>
 A:Cross-references: GB:U52074; NID:g1326148; PIDN:AAB40903.1; PID:g1326149

A:Accession: PC4315
 A:Molecule type: protein
 A:Residues: 37-43;142-148 <TSU2>
 C:Comment: This receptor is involved in the initial adhesive interaction between lymph
 sites of inflammation.
 C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology
 F:1-38/Domain: signal sequence #status predicted <Sig>
 F:39-155/Domain: C-type lectin homology <LCH>
 F:39-372/Product: L-selectin #status predicted <MAT>
 F:39-157/Domain: calcium-binding #status predicted <CAB>
 F:160-191/Domain: EGF homology <EGF>
 F:197-254/Domain: complement factor H repeat homology <FHI>
 F:259-316/Domain: complement factor H repeat homology <FHI2>
 F:333-355/Domain: transmembrane #status predicted <TM>
 F:356-372/Domain: intracellular #status predicted <INT>

Query Match 94.1%; Score 1992; DB 2; Length 372;
 Best local Similarity 93.5%; Pred. No. 8,9e-141;
 Matches 348; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 MIFPMKQSTORDLWNIIFKLMGWTMLCDPLAHGTYCWTYHSEKPMNQARRCRDN 60
 DB 1 MIFPMKQSTORDLWNIIFKLMGWTMLCDPLAHGTYCWTYHSEKPMNQARRCRDN 60
 QY 61 YTDVLAIONKAELEYEKLTPESRSYTWGIRKIGIMTWGNTKSLTEAEWNGGEPRN 120
 DB 61 YTDVLAIONKAELEYEKLTPESRSYTWGIRKIGIMTWGNTKSLTEAEWNGGEPRN 120
 QY 121 NKNKEDCEYIYIKRNKDGKWNDDACHKRLKALCYTASCPWMSGHGECEIINNTTC 180
 DB 121 NKNKEDCEYIYIKRNKDGKWNDDACHKRLKALCYTASCPWMSGHGECEIINNTTC 180
 QY 181 NCDVGYGQCQVLVIOCEPLEPELGTMDCTHPFNGFSSSCAFSCSEGTNLGIEETT 240
 DB 181 NCDVGYGQCQVLVIOCEPLEPELGTMDCTHPFNGFSSSCAFSCSEGTNLGIEETT 240
 QY 241 CGPFGMWSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSPSACFTICSEGTNLGIEETT 300
 DB 241 CGPFGMWSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSPSACFTICSEGTNLGIEETT 300
 QY 301 TICSSGIMSNPSPICQKLDKSFMSIKEDGYNPLFIPAVVMTAFSGLAFTIIMLARLKK 360
 DB 301 TICSSGIMSNPSPICQKLDKSFMSIKEDGYNPLFIPAVVMTAFSGLAFTIIMLARLKK 360
 QY 361 GKSKRSMDPY 372
 DB 361 GKSKRSMDPY 372

RESULT 3
 JC4892
 L-selectin precursor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Accession: JC4892
 C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 21-Jan-2000
 R:Qian, J.; Huang, X.; Marks, R.M.
 A:Title: Cloning of the cDNA for rabbit L-selectin and expression of recombinant prot
 A:Reference number: JC4892; MUID:96354800
 A:Accession: JC4892
 A:Molecule type: mRNA
 A:Residues: 1-376 <QIA>
 A:Cross-references: GB:U26335; NID:g847787; PIDN:AA67896.1; PID:g847788
 C:Comment: This protein involved in leukocyte-endothelial adhesion; it mediates adhes
 C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology
 F:1-37/Domain: signal sequence #status predicted <Sig>
 F:38-376/Product: L-selectin #status predicted <MAT>
 F:160-191/Domain: EGF homology <EGF>
 F:197-254/Domain: complement factor H repeat homology <FHI>
 F:259-316/Domain: transmembrane #status predicted <TM>

[illegible]

Db 241 CGASNMWYLEPICQVIOCMPLADLGTMECSHPLANFSFTACTFTCTSEEDLIGERRK 300
 QY 301 TICESGSIWNSPICKOKLDKSFMSIKSGDYNPFLTPAVWMTATSGAFLIIMARRKK 360
 Db 301 TYCRSSGMSSPICQTKRSFKIKSGDYNFLTPAVWMTATSGAFLIIMARRKK 360
 QY 361 GKSKSRSMNDPY 372
 Db 361 GKSKSRSMNDPY 372

RESULT 6

L-selectin precursor, short splice form - human
 L-Alternat names: CB62L; leucocyte cell adhesion molecule-1 (LECAM-1, LAM-1); leukocyte
 ral lymph node homing receptor Leu-8
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 26-May-2000
 C:Accession: S09702
 R:Cammerlin, D.; James, S.P.; Stamenkovic, I.; Seed, B.
 Nature 342, 78-82, 1989
 A:Title: Leu-8/701 is the human equivalent of the Mel-14 lymph node homing receptor.
 A:Reference number: S06798; MUID:90044046
 A:Accession: S09702
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-323 <CAM>
 A:Cross-references: EMBL:X17519; NID:934344
 A:Note: this translation is not annotated in Genbank entry HSEU8, release 111.0
 C:Comment: For an alternative splice form, see PIR:A34015.
 C:Genetics:
 A:Gene: GDB:SELL; GDB:LNHR; LSEL; LAM1; LYAM1; LAN-1
 A:Cross-references: GDB:120157; GDB:118834; OMIM:153240
 A:Map position: 1922-1923
 A:Introns: 14/3; 42/1; 171/1; 207/1; 269/1; 303/2
 C:Function:
 A:Description: binds with low affinity to oligosaccharides like heparan sulfate and sialy
 ment of leucocytes to areas of inflammation, and with CD162 mediates neutrophil-neutroph
 C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology;
 C:Keywords: alternative splicing; cell adhesion; duplication; glycoprotein; inflammation
 F:1-51/Domain: signal sequence #status predicted <SIG>
 F:42-168/Domain: C-type lectin homology <LCH>
 F:52-323/Product: L-selectin #status predicted <EXT>
 F:52-300/Domain: extracellular #status predicted <EXT>
 F:173-204/Domain: EGF homology <EGF>
 F:210-267/Domain: complement factor H repeat homology <PH1>
 F:272-323/Domain: complement factor H repeat homology #status atypical <FH2>
 F:301-318/Domain: transmembrane #status predicted <TM>
 F:319-323/Domain: intracellular #status predicted <INT>
 F:73,117,190,245,259/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:322/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 78.1%; Score 1652; DB 1; Length 323;
 Best Local Similarity 98.3%; Pred. No. 1.4e-115;
 Matches 285; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIFPMKCGSTQBDLWNIFKLMGWTMLCDPLAHGHTYCTYHYSEKPMWQARRFCRDN 60
 Db 14 MIFPMKCGSTQBDLWNIFKLMGWTMLCDPLAHGHTYCTYHYSEKPMWQARRFCRDN 73
 QY 61 YTDVAIONKAELEYLEKTLPSRSYTWGIRKIGIWTWGTNKSLEAEANMGDGEPN 120
 Db 74 YTDVAIONKAELEYLEKTLPSRSYTWGIRKIGIWTWGTNKSLEAEANMGDGEPN 133
 QY 121 NKKNKEDCEYIYIKRNKDGKWNDDACHIKRALCYTASCPWMSGGEGCEIINNNTC 180
 Db 134 NKKNKEDCEYIYIKRNKDGKWNDDACHIKRALCYTASCPWMSGGEGCEIINNNTC 193
 QY 181 NCDVGYGPOCOLVQCEPLAELGTMDCTHPFGNFSFSSQCAFCSEGTNLGTIEETT 240
 Db 194 NCDVGYGPOCOLVQCEPLAELGTMDCTHPFGNFSFSSQCAFCSEGTNLGTIEETT 253

QY 241 CGPGRNMSPEPTICQVIOCEPLASPDLTGTMCSHPLASFTSACTFTCS 290
 Db 254 CGPGRNMSPEPTICQVIOCEPLASPDLTGTMCSHPLASFTSACTFTCS 303

RESULT 7

L-selectin precursor - mouse
 L-Alternat names: lymph node homing receptor MEL-14; lymphocyte surface antigen Ly-2
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
 C:Accession: A32375; A35102; A40167; A60906
 R:Laskey, L.A.; Singer, M.S.; Yednock, T.A.; Dowbenko, D.; Fennie, C.; Rodriguez, H.;
 Cell 56, 1045-1055, 1989
 A:Title: Cloning of a lymphocyte homing receptor reveals a lectin domain.
 A:Reference number: A32375; MUID:89168433
 A:Accession: A32375
 A:Molecule type: mRNA
 A:Residues: 1-372 <LAS>
 A:Cross-references: GB:M25324; NID:g198803; PIDN:AAA39431.1; PID:g198804
 R:Siegelman, M.H.; Cheng, I.C.; Weissman, I.L.; Wakeland, E.K.
 Cell 61, 611-622, 1990
 A:Title: The mouse lymph node homing receptor is identical with the lymphocyte cell s
 A:Reference number: A35102; MUID:90263086
 A:Accession: A35102
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-372 <SIE>
 A:Cross-references: GB:M36005; NID:g199735; PIDN:AAA39722.1; PID:g199736; GB:M36058;
 R:Siegelman, M.H.; van de Rijn, M.; Weissman, I.L.
 Science 243, 1165-1172, 1989
 A:Title: Mouse lymph node homing receptor cDNA clone encodes a glycoprotein revealing
 A:Reference number: A40167; MUID:89162048
 A:Accession: A40167
 A:Molecule type: mRNA
 A:Residues: 1-372 <SIE>
 A:Cross-references: GB:X14772; NID:g52942; PIDN:CAA32880.1; PID:g52943
 A:Note: part of this sequence, including the amino end of the mature protein, was con
 R:Siegelman, M.; Bond, M.W.; Gallatin, W.M.; St. John, T.; Smolth, H.T.; Fried, V.A.; W
 Science 231, 823-829, 1986
 A:Title: Cell surface molecule associated with lymphocyte homing is a ubiquitinated b
 A:Reference number: A60906; MUID:86122900
 A:Accession: A60906
 A:Molecule type: protein
 A:Residues: 'X', '40', 'Y', '42', 'XXX', '46', 'Y', '48', 'XXXXXX', '55-56', 'X', '58', 'XXXXXX', '65', 'V', '67', 'X
 C:Comment: This protein is ubiquitinated.
 C:Function:
 A:Description: binds with low affinity to oligosaccharides like heparan sulfate and si
 ment of leucocytes to areas of inflammation, and with CD162 mediates neutrophil-neutr
 C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homolog
 C:Keywords: cell adhesion; duplication; glycoprotein; inflammation; phosphoprotein; s
 F:1-38/Domain: signal sequence #status predicted <SIG>
 F:129-155/Domain: C-type lectin homology <LCH>
 F:39-372/Product: L-selectin #status experimental <NAT>
 F:39-331/Domain: extracellular #status predicted <EXT>
 F:160-191/Domain: EGF homology <EGF>
 F:197-254/Domain: complement factor H repeat homology <PH1>
 F:259-316/Domain: complement factor H repeat homology <PH2>
 F:332-355/Domain: transmembrane #status predicted <TM>
 F:356-372/Domain: intracellular #status predicted <INT>
 F:60,104,216,246,278,308,320/Binding site: carboxylate (Asn) (covalent) #status pred
 F:364/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 78.0%; Score 1651; DB 1; Length 372;
 Best Local Similarity 76.1%; Pred. No. 1.9e-115;
 Matches 283; Conservative 32; Mismatches 57; Indels 0; Gaps 0;

QY 1 MIFPMKCGSTQBDLWNIFKLMGWTMLCDPLAHGHTYCTYHYSEKPMWQARRFCRDN 60
 Db 1 MIFPMKCGSTQBDLWNIFKLMGWTMLCDPLAHGHTYCTYHYSEKPMWQARRFCRDN 60
 QY 61 YTDVAIONKAELEYLEKTLPSRSYTWGIRKIGIWTWGTNKSLEAEANMGDGEPN 120

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Db 61 YTDVAIQNKRELEYLENTLPKSPYIYTWIGIRKIGKMMWVGINKITLKEHNMAGEPN 120
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 121 NKNKEDCEVIYIKRNKADKWDNDACHIKLKAALCYTASCPWSCSGHGECEIINNHTC 180
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 121 NKSKECEVEIYIKREDSKWDNDACHIKRKAALCYTASCPGSCNGRGEVEIINNHTC 180
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 181 NCDVGYIQCQVLYOCEPLLEAPELGTMDCTHPFGNFSFSCAFSCSEGTNLGTIEETT 240
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 181 ICAGYGYPCQVYVOCPELEAPELGTMDCIHPLGNFSFSCAFNCSSEGRRLGTAEQ 240
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 241 CGPFGNMSPEPTQVYQCEPLSAPDLGINMCSHPLASFSTSACTFCSGEETLICKKK 300
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 241 CGASGNMSSPEPTQVYQCEPLLEAPELGTMDCIHPLGNFSFSCAFNCSSEGRRLGTAE 300
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 301 TICSSGIMNSPFIQCKLKSFSMEKGDYNPFLIPAVVTAFAISLAFIIMLARLKK 360
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 301 TCGASGNMSSPEPTQVYQCEPLLEAPELGTMDCIHPLGNFSFSCAFNCSSEGRRLGTAE 360
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 361 GKRSKRMNDPY 372
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 361 GKRSKRMNDPY 372
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 8
A30359
P-selectin precursor - human
N:Alternate names: CD62 antigen; granule membrane protein 140
C:Species: Homo sapiens (man)
C>Date: 18-Oct-1989 #sequence_revision 30-Sep-1991 #text_change 19-May-2000
C:Accession: A30359
R:Johnson, G.I.; Cook, R.G.; McEwen, R.P.
Cell 56, 1033-1044, 1989
A:Title: Cloning of GMP-140, a granule membrane protein of platelets and endothelium: se
A:Reference number: A30359; MUID:89168432
A:Accession: A30359
A:Molecule type: mRNA
A:Residues: 1-830 <TOH>
A:Cross-references: GB:M25322
A:Note: parts of this sequence, including the amino end of the mature protein, were conf
C:Genetics:
A:Gene: GDB:SELP; GRMP
A:Cross-references: GDB:120018; OMIM:173610
A:Map position: 1q22-1q25
C:Superfamily: unassigned EGF-related proteins; complement factor H repeat homology; EGF
C:Keywords: cell adhesion; glycoprotein; phosphohistidine; phosphoprotein; surface anti
F:1-41/Domain: signal sequence #status predicted <Sig>
F:42-630/Product: P-selectin #status experimental <MAT>
F:163-194/Domain: EGF homology <EGF>
F:200-257/Domain: complement factor H repeat homology <FH01>
F:262-319/Domain: complement factor H repeat homology <FH02>
F:324-381/Domain: complement factor H repeat homology <FH03>
F:386-443/Domain: complement factor H repeat homology <FH04>
F:448-505/Domain: complement factor H repeat homology <FH05>
F:510-567/Domain: complement factor H repeat homology <FH06>
F:572-629/Domain: complement factor H repeat homology <FH07>
F:642-699/Domain: complement factor H repeat homology <FH08>
F:704-761/Domain: complement factor H repeat homology <FH09>
F:772-795/Domain: transmembrane #status predicted <TMN>
F:796-830/Domain: intracellular #status predicted <CYT>
F:54,98,180,212,219,411,460,518,665,716,723,741/Binding site: carbohydrate (Asn) (coval
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Db 71 ONKNEIDYLNKVLBYSSYYWIGIRKNNKTWTYGTCKALTNENADNEPNKKRNED 130
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 128 CVEIYIKRNKADKWDNDACHIKLKAALCYTASCPWSCSGHGECEIINNHTCNDVGY 187
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 131 CVEIYIKSPAPKGNDEHCLKKHAALCYTASCPDSCSKSGELETIGNTCSCPGFY 190
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 188 GPQCQLYQCEPLLEAPELGTMDCTHPFGNFSFSCAFSCSEGTNLGTIEETTGPFGNW 247
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 191 GPECEYRECELELPHVLMNCSHPPLGNFSFNQCSFHTDGYQVNGPSKLECLASGIW 250
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 248 SSPEPTQVYQCEPLSAPDLGINMCSHPLASFSTSACTFCSGEETLICKKKTCSSG 307
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 251 TKNPQCLAAQCPLPKRPGNMICLSAKAFQHOSSCSCEGFAVQPEVYQCTASG 310
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 308 TWSNPSPICQ 317
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 311 VWTAPAPVCK 320
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
```

```
RESULT 9
A42755
P-selectin precursor - mouse
N:Alternate names: CD62; granule membrane protein 140; PADGEM
C:Species: Mus musculus (house mouse)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 19-May-2000
C:Accession: A42755; A44899
R:Weller, A.; Isenmann, S.; Vestweber, D.
J. Biol. Chem. 267, 15176-15183, 1992
A:Title: Cloning of the mouse endothelial selectins. Expression of both E- and P-sele
A:Reference number: A42755; MUID:92340571
A:Accession: A42755
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-768 <MBL>
A:Cross-references: GB:M8761; NID:g200552; PIDN:AAA0008.1; PID:g200553
A:Experimental source: endothelial cells
A:Note: sequence extracted from NCBI backbone (NCBIP:109467)
R:Sanders, W.E.; Wilson, R.W.; Ballantyne, C.M.; Beaudet, A.L.
Blood 80, 795-800, 1992
A:Title: Molecular cloning and analysis of in vivo expression of murine P-selectin.
A:Reference number: A44899; MUID:92345617
A:Accession: A44899
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-723, '725-768 <SAN>
A:Cross-references: GB:M72332; NID:g193565; PIDN:AAA37712.1; PID:g193566
A:Note: sequence extracted from NCBI backbone (NCBIP:109900)
C:Superfamily: unassigned EGF-related proteins; complement factor H repeat homology;
C:Keywords: cell adhesion; glycoprotein; phosphohistidine; phosphoprotein; transmembr
F:1-41/Domain: signal sequence #status predicted <Sig>
F:42-768/Product: P-selectin #status predicted <MAT>
F:163-194/Domain: EGF homology <EGF>
F:200-257/Domain: complement factor H repeat homology <FH01>
F:262-319/Domain: complement factor H repeat homology <FH02>
F:324-381/Domain: complement factor H repeat homology <FH03>
F:386-443/Domain: complement factor H repeat homology <FH04>
F:448-505/Domain: complement factor H repeat homology <FH05>
F:510-567/Domain: complement factor H repeat homology <FH06>
F:580-637/Domain: complement factor H repeat homology <FH07>
F:642-699/Domain: complement factor H repeat homology <FH08>
F:710-733/Domain: transmembrane #status predicted <TMN>
F:734-768/Domain: intracellular #status predicted <INT>
F:45,54,107,212,347,398,456,467,603,654,661,679/Binding site: carbohydrate (Asn) (cov
```

```
Query Match 42.8%; Score 905; DB 2; Length 830;
Best Local Similarity 50.6%; Pred. No. 1.1e-59;
Matches 157; Conservative 47; Mismatches 106; Indels 0; Gaps 0;

Qy 8 QSNQRODLMNFKMGWMLCCDPLAHNGTCTWYHYSEKPMNORARPCRDNTDVAI 67
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 11 QNRQRRVFGISQLSCFALLSELTKNOKEVAAWYHSTKAYSNWISKRYQNRRTDVAI 70
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Qy 68 QNKAIEIYLEKTPFSRSYWGIRKIGIIMTWGNTKSLTEAENNGDEPNKKRNED 127
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
```

```
Query Match 42.7%; Score 902.5; DB 2; Length 768;
Best Local Similarity 52.0%; Pred. No. 1.6e-59;
Matches 156; Conservative 40; Mismatches 103; Indels 1; Gaps 1;

Qy 20 LMGWMLCCDPLAHNGTCTWYHYSEKPMNORARPCRDNTDVAIQKAEIYLEKT 79
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 24 IWFSAIISLVNOKKEVAAWYHSTKAYSNWISKRYQNRRTDVAIQKNEIAHLNDV 82
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
```


A:Reference number: A35046; MUID:90175359
A:Accession: A35046
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-610 <HES>
A:Cross-references: GB:R30640; NID:g182047; PID:AA52377.1; PID:g182048
R:Bevilacqua, M.P.; Stengelin, S.; Gimbrone Jr., M.A.; Seed, B.
Science 243, 1160-1165, 1989
A>Title: Endothelial leukocyte adhesion molecule 1: an inducible receptor for neutrophils
A:Reference number: A32606; MUID:89162047
A:Accession: A32606
A:Molecule type: mRNA
A:Residues: 1-467, 'Y', 469-610 <BEV>
A:Cross-references: GB:M2436; NID:g537523; PID:AA52376.1; PID:g537524
C:Genetics:
A:Gene: GDB:SELE; ELAM; ESEL; ELAM1
A:Cross-references: GDB:120612; OMIM:131210
A:Map position: 1q22-1q25
C:Superfamily: unassigned EGF-related proteins; C-type lectin homology; complement factor
C:Keywords: duplication; signal sequence #status predicted tandem repeat; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <CH>
F:12-138/Domain: C-type lectin homology <CH>
F:12-610/Product: endothelial leukocyte adhesion molecule 1 #status predicted <MAT>
F:143-174/Domain: EGF homology <EGF>
F:180-237/Domain: complement factor H repeat homology <FH01>
F:242-299/Domain: complement factor H repeat homology <FH02>
F:304-362/Domain: complement factor H repeat homology <FH03>
F:367-428/Domain: complement factor H repeat homology <FH04>
F:430-485/Domain: complement factor H repeat homology <FH05>
F:493-547/Domain: complement factor H repeat homology <FH06>
F:557-578/Domain: transmembrane #status predicted <TM>
F:55-145,160,179,199,200,265,312,332,503,527/Binding site: carbohydrate (Asn) (covalently

A/Note: the sequence in GenBank entry MUSELEEC, release 117.0, (PID:AAA37577.1; PID:94
 A/Note: it is uncertain whether the initiator is Met-1 or the AUG codon preceding that
 C:Superfamily: unassigned EGF-related proteins; C-type lectin homology; complement factor
 C/keywors: glycoprotein; transmembrane protein
 F:1-21/Domain: C-type lectin homology <LCH>
 F:12-138/Domain: C-type lectin homology <LCH>
 F:22-612/Product: P-selectin #status predicted <MAT>
 F:143-174/Domain: EGF homology <EGF>
 F:180-238/Domain: complement factor H repeat homology <FH1>
 F:243-300/Domain: complement factor H repeat homology <FH2>
 F:305-363/Domain: complement factor H repeat homology <FH3>
 F:368-426/Domain: complement factor H repeat homology <FH4>
 F:431-489/Domain: complement factor H repeat homology <FH5>
 F:494-548/Domain: complement factor H repeat homology <FH6>
 F:525,591,528/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.5%; Score 857; DB 2; Length 612;
 Best Local Similarity 51.4%; Pred. No. 3e-56;
 Matches 148; Conservative 42; Mismatches 96; Indels 2; Gaps 2;

QY 31 LAHGTWCWTHYSEKPMNQRARPCRDNYTLVAIONKAETLEYLTKLPFSRSTYWG 90
 DB 15 LAGEST-AMTYNASSSELMTYDEASATCQRDYTHLVAIONKEELYNLSNLKHSPTYYWG 73
 QY 91 IRRIGGIWTVGTNKSILTEEAENMGDEPNKKKEDCVETIYIKRNKAGKNDACAKL 150
 DB 74 IRKYNVNWIMVIGKPLTEBAQNAWAPERNKRNEDCVETIYIORTKDSGMNDEKCNK 133
 QY 151 KAALCTYASCQPMSCSGHGEVETIINNHTCNCVGYGQCLVIOCEPLAPDELGTMD 210
 DB 134 KIALCTYASTNASCSCGHGECITFINSYCKCHPGFPCNCEQAVYCKPQEHDPYGSINC 193
 QY 211 THPEGNFSSQCAFCSSETNLTGIEET-CCPFQWSSPEPTCOVIOCEPLAPDLGI 269
 DB 194 SHPEGPFSTNSSCSFGCKRGLPSSMETTYRCSSGEMSAAPACHAVECEALTHPAHGI 253
 QY 270 MNCSHPLASFSTACTFICSEGTETLIGKKITICSSGIMNSPICO 317
 DB 254 RKCSNPGSYPMWNTCTCFDCEYRRVGAQNLCTSSGIMDNFTPSCK 301

RESULT 15
 S36772
 E-selectin - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 19-May-2000
 C:Accession: S36772
 R:Nguyen, M.; Scrudell, N.A.; Bischoff, J.
 Nature 365, 267-269, 1993
 A>Title: A role for sialyl Lewis-X/A glycoconjugates in capillary morphogenesis.
 A:Reference number: S36772; MUID:93382537
 A:Accession: S36772
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-485 <NGD>
 A:Cross-references: GB:U12039; NID:9402913; PID:AAA02991.1; PID:9402914
 C:Superfamily: unassigned EGF-related proteins; C-type lectin homology; complement factor
 F:13-139/Domain: C-type lectin homology <LCH>
 F:181-237/Domain: complement factor H repeat homology <FH1>
 F:242-299/Domain: complement factor H repeat homology <FH2>
 F:304-362/Domain: complement factor H repeat homology <FH3>
 F:367-421/Domain: complement factor H repeat homology <FH4>

Query Match 40.1%; Score 849.5; DB 2; Length 485;
 Best Local Similarity 53.0%; Pred. No. 8.6e-56;
 Matches 148; Conservative 40; Mismatches 90; Indels 1; Gaps 1;

QY 39 WTHYHSEKPMNQRARPCRDNYTLVAIONKAETLEYLTKLPFSRSTYWGIRKIGTW 98
 DB 23 WSHYHSEKPMNQRARPCRDNYTLVAIONKAETLEYLTKLPFSRSTYWGIRKIGTW 82

QY 99 TWVGTNKSILTEEAENMGDEPNKKKEDCVETIYIKRNKAGKNDACAKLKAALCTYA 158
 DB 83 TWIGTNSLTKKATNNAPERNKQSDCEVETIYIKRSDSGKWNDEKTKQKALACTYA 142
 QY 159 SCQPMSCSGHGEVETIINNHTCNCVGYGQCLVIOCEPLAPDELGTMDCTHPGNFS 218
 DB 143 ACNPTFCGSHGECVETIINNHTCNCVGYGQCLVIOCEPLAPDELGTMDCTHPGNFS 201
 QY 219 FSSQCAFCSSETNLTGIEETTCGPFQWSSPEPTCOVIOCEPLAPDLGIIMNSHPLAS 278
 DB 202 YNSSCSISCAEGYLPSTETATRCMSSGEMSTPLPKCNVACDLASMDNGVANCSPNHGS 261
 QY 279 FSTFSACTFICSEGTETLIGKKITICSSGIMNSPICO 317
 DB 262 LPWNTCTCFDCEYRRVGAQNLCTSSGIMDNFTPSCK 300

Search completed: October 13, 2001, 02:55:06
 Job time: 4208 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2001, 02:54:03 ; Search time 53.96 Seconds
(without alignments)
236.157 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116

Sequence: 1 MIFPMKCGSTGRDLNIFKL.....WLARRLKGGKSKSRMNDPY 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2090	98.8	372	1	LEM1_HUMAN
2	2085	98.5	372	1	LEM1_PANTR
3	2062	97.4	372	1	LEM1_PONPY
4	1996	94.3	372	1	LEM1_MACMU
5	1992	94.1	372	1	LEM1_PAPHA
6	1682	79.5	370	1	LEM1_BOVIN
7	1651	78.0	372	1	LEM1_RAT
8	1651	78.0	372	1	LEM1_MOUSE
9	919.5	43.5	769	1	LEM3_SHEEP
10	905	42.8	830	1	LEM3_HUMAN
11	902.5	42.7	768	1	LEM3_MOUSE
12	894.5	42.3	646	1	LEM3_BOVIN
13	885	41.8	768	1	LEM3_RAT
14	862	40.7	610	1	LEM2_HUMAN
15	861	40.6	551	1	LEM2_RABIT
16	860	40.6	611	1	LEM2_CANFA
17	858.5	40.6	549	1	LEM2_RAT
18	857	40.5	612	1	LEM2_MOUSE
19	849.5	40.1	485	1	LEM2_BOVIN
20	814.5	38.5	484	1	LEM2_PIG
21	212.5	10.0	1019	1	LFC_TACTR
22	199.5	9.4	1231	1	CFAH_HUMAN
23	195	9.2	958	1	HIG_DROME
24	189.5	9.0	1019	1	LFC_CARRO
25	172	8.1	2039	1	CRI_HUMAN
26	171	8.1	2333	1	PGCA_CANFA
27	168	7.9	2132	1	PGCA_MOUSE
28	167	7.9	331	1	FCE2_HUMAN
29	167	7.9	1234	1	CFAB_MOUSE
30	166.5	7.9	558	1	C4BP_MOUSE
31	166	7.8	390	1	DAPI_MOUSE
32	166	7.8	1456	1	MANR_HUMAN
33	166	7.8	2364	1	PGCA_BOVIN

34	165	7.8	311	1	LECI_HUMAN	P07307	homo sapien
35	165	7.8	548	1	KUCR_MOUSE	P70194	rattus musculu
36	163	7.7	2124	1	PGCA_RAT	P07897	rattus norv
37	162.5	7.7	345	1	APOH_BOVIN	P17650	bos taurus
38	162	7.7	304	1	MMGL_MOUSE	P49300	mus musculu
39	160	7.6	2415	1	PGCA_HUMAN	P61312	homo sapien
40	157	7.4	331	1	FCE2_MOUSE	P20693	mus musculu
41	157	7.4	469	1	C4BP_MOUSE	P08607	mus musculu
42	157	7.4	610	1	C4BP_BOVIN	P28065	bos taurus
43	156.5	7.4	207	1	LECH_CHICK	P02707	gallus gall
44	156.5	7.4	1025	1	CR2_MOUSE	P19070	mus musculu
45	156	7.4	258	1	C4BP_RAT	P06315	rattus norv

ALIGNMENTS

RESULT 1
LEM1_HUMAN STANDARD; PRT; 372 AA.
ID
AC P14151; P15023;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).
DE SEL1 OR LYAM1 OR LNH1.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=89315837; PubMed=2664786;
RA Siegelman M.H., Weissman I.L.;
RT "Human homologue of mouse lymph node homing receptor: evolutionary conservation at tandem cell interaction domains";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5562-5566(1989).
RN [2]
RP MEDLINE=9310350; PubMed=2473156;
RA Tedder T.F., Isaacs C.M., Ernst T.J., Demetri G.D., Adler D.A., Distche C.W.;
RT "Isolation and chromosomal localization of cDNAs encoding a novel human lymphocyte cell surface molecule, LAM-1. Homology with the mouse lymphocyte homing receptor and other human adhesion proteins.";
RL J. Exp. Med. 170:123-133(1989).
RN [3]
RP MEDLINE=90044046; PubMed=2509939;
RA Camerini D., James S.P., Stamenkovic I., Seed B.;
RT "Leu-8/TQ1 is the human equivalent of the Mel-14 lymph node homing receptor";
RL Nature 342:78-82(1989).
RN [4]
RP MEDLINE=9308881; PubMed=2663882;
RA Bowen B.R., Nguyen T., Lasky L.A.;
RT "Characterization of a human homologue of the murine peripheral lymph node homing receptor";
RL J. Cell Biol. 109:421-427(1989).
RN [5]
RP MEDLINE=90243637; PubMed=1692315;
RA Ord D.C., Ernst T.J., Zhou L.J., Rambaldi A., Spertini O., Griffith J., Tedder T.F.;
RT "Structure of the gene encoding the human leukocyte adhesion molecule-1 (TQ1, Leu-8) of lymphocytes and neutrophils";
RL J. Biol. Chem. 265:7760-7767(1990).
RN [6]
RP 3D-STRUCTURE MODELING.

Query Match	Best Local Similarity	Score 2090;	DB 1;	Length 372;
Matches 368;	Conservative 1;	Mismatches 3;	Indels 0;	Gaps 368;
QY 1 MIFPKCOSTQTDRLMNIFFKLMGWTMLCDPFLAHGTYCWTYHSEKPMNORARRCRDN 60	98.8%;	98.9%;	DB 1;	Length 372;
Db 1 MIFPKCOSTQTDRLMNIFFKLMGWTMLCDPFLAHGTYCWTYHSEKPMNORARRCRDN 60				
QY 61 YTDVAIONKAEIIEYLEKTLPPSRSYWIGIRKIGGIWTVGWNKSLTEBAENMGDGEPN 124				
Db 61 YTDVAIONKAEIIEYLEKTLPPSRSYWIGIRKIGGIWTVGWNKSLTEBAENMGDGEPN 124				
QY 121 NKKKKECCVEIYIKRKKDKGKNNDDACKHKLAAALCYTASQCPMSSCGSHGECVEIINNHTC 180				
Db 121 NKKKKECCVEIYIKRKKDKGKNNDDACKHKLAAALCYTASQCPMSSCGSHGECVEIINNHTC 180				
QY 181 NCDVGYGPPCOOLVIOCEPLEAELGTMDCTHPFGNSSFSSQCAFCSGEGTMTGIEETT 240				
Db 181 NCDVGYGPPCOOLVIOCEPLEAELGTMDCTHPFGNSSFSSQCAFCSGEGTMTGIEETT 240				
QY 241 CGPFGMNSSPEPFCQYTOCEPLSADGLTMCNCSHPLASFSFISACFFISBETELIGRKK 300				
Db 241 CGPFGMNSSPEPFCQYTOCEPLSADGLTMCNCSHPLASFSFISACFFISBETELIGRKK 300				
QY 301 TICSSGIMNSPFCIOKLDKFSFKIRGVDNPLFTIVAAWTAFAAGLAFITMLARRKK 360				
Db 301 TICSSGIMNSPFCIOKLDKFSFKIRGVDNPLFTIVAAWTAFAAGLAFITMLARRKK 360				
QY 361 GKSKSRSMNDPY 372				
Db 361 GKSKSRSMNDPY 372				
RESULT 2				
LEMI_PANTR	STANDARD;	PRT;	372 AA.	
AC G95237;				
DT 01-NOV-1997 (Rel. 35, Created)				
DT 01-NOV-1997 (Rel. 35, Last sequence update)				
DT 01-NOV-1997 (Rel. 35, Last annotation update)				
L-SELECTIN PRECURSOR (L1MPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (UAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).				
DE MOLECULE-1) (UAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).				
GN SELL.				
OC Pan troglodytes (Chimpanzee).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.				
NCBI_TaxId=9598;				
XP (1)				
SEQUENCE FROM N.A.				
Budman J.I., Fu H., Johnson C.E., Thakur A.B., Berg E.L.				

RA Tsurushita N.;
 RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADHERENCE
 CC OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
 CC VENULES IN PERIPHERAL LYMPH NODES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U73729; AAB18248.1; -
 CC HSSP: P14151; IKJB.
 DR InterPro: IPR000436; -
 DR InterPro: IPR000561; -
 DR InterPro: IPR001304; -
 DR InterPro: IPR002396; -
 DR Pfam: PF00008; EGF_1.
 DR Pfam: PF00059; lectin_c; 1.
 DR Pfam: PF00084; sush1; 2.
 DR PRINTS: PRO0343; SELECTIN.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00615; C-TYPE-LECTIN_1; 1.
 DR PROSITE: PS50041; C-TYPE-LECTIN_2; 1.
 DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
 KW Selectin; Signal; Sush1; Repeat.
 FT SIGNAL 1 28
 FT PROPEP 29 38
 FT CHAIN 39 372
 FT DOMAIN 39 332
 FT TRANSMEM 333 355
 FT DOMAIN 356 372
 FT DOMAIN 55 155
 FT DOMAIN 156 192
 FT DOMAIN 196 317
 FT DOMAIN 196 255
 FT DOMAIN 258 317
 FT DISULFID 57 155
 FT DISULFID 128 147
 FT DISULFID 160 171
 FT DISULFID 165 180
 FT DISULFID 182 191
 FT DISULFID 197 241
 FT DISULFID 227 254
 FT DISULFID 259 303
 FT CARBOHYD 289 316
 FT CARBOHYD 60 60
 FT CARBOHYD 104 104
 FT CARBOHYD 177 177
 FT CARBOHYD 216 216
 FT CARBOHYD 232 232
 FT CARBOHYD 246 246
 FT CARBOHYD 271 271
 SQ SEQUENCE 372 AA: 42188 MW: 6EA9J1802A2D3643 CRC64;

Query Match 98.5%; Score 2085; DB 1; Length 372;
 Best Local Similarity 98.7%; Pred No. 1e-162;
 Matches 367; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFFPKGQSTORDLWNIFFKLGWTLMLCDFLAHGTYCPTYHYSEKPMNQARARECRDN 60
 DB 1 MFFPKGQSTORDLWNIFFKLGWTLMLCDFLAHGTYCPTYHYSEKPMNQARARECRDN 60

QY 61 YFDLVALIONKAELELEYEKTLPFSRSYYWIGIRKIGGIWTVGNKSLTEBAEMNGOSEPN 120
 DB 61 YFDLVALIONKAELELEYEKTLPFSRSYYWIGIRKIGGIWTVGNKSLTEBAEMNGOSEPN 120
 QY 121 NKKNKEDCEVETIYIKRNKNDAGKAMDACCHKLKAALCTASCPMSGSGHGEVEIINNHTC 180
 DB 121 NKKNKEDCEVETIYIKRNKNDAGKAMDACCHKLKAALCTASCPMSGSGHGEVEIINNHTC 180
 QY 181 NCDVGYGGPQCQVLVIOCEPLEDELGTMDCTHPFGNFSSSGCAFSCSEGTNLGTLEETT 240
 DB 181 NCDVGYGGPQCQVLVIOCEPLEDELGTMDCTHPFGNFSSSGCAFSCSEGTNLGTLEETT 240
 QY 241 CGFPGWMSSEPPRCQVYIQCEPLASAPDLGTWNCSHPLASFSTACPFICSEGTLEIGKK 300
 DB 241 CGFPGWMSSEPPRCQVYIQCEPLASAPDLGTWNCSHPLASFSTACPFICSEGTLEIGKK 300
 QY 301 TIESSGIMNSPSPICOKLDRSFMKEGDNPLFTPVAVMTAFSGLAFTIWLARLKK 360
 DB 301 TIESSGIMNSPSPICOKLDRSFMKEGDNPLFTPVAVMTAFSGLAFTIWLARLKK 360
 QY 361 GKSKRSMDPY 372
 DB 361 GKSKRSMDPY 372
 RESULT 3
 LEM1_PONPY STANDARD; PRT; 372 AA.
 AC 095235;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION
 DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1)
 DE (LECAM1) (CD62L).
 GN SELL.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
 OC NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Budman J.I., Fu H., Johnson C.E., Thakur A.B., Berg E.L.,
 RA Tsurushita N.;
 RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADHERENCE
 CC OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
 CC VENULES IN PERIPHERAL LYMPH NODES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U73729; AAB18247.1; -
 CC HSSP: P14151; IKJB.
 DR InterPro: IPR000436; -
 DR InterPro: IPR000561; -
 DR InterPro: IPR001304; -
 DR InterPro: IPR002396; -
 DR Pfam: PF00008; EGF_1.
 DR Pfam: PF00059; lectin_c; 1.
 DR Pfam: PF00084; sush1; 2.
 DR PRINTS: PRO0343; SELECTIN.
 DR PROSITE: PS00022; EGF_1; 1.

Query Match	97.48;	Score 2062;	DB 1;	Length 372;
Best Local Similarity	97.68;	Pred. No. 7.5e-161;		
Matches 363; Conservative	5;	Mismatches 4;	Indels 0;	Gaps 0

RESULT	4	
LEMI_MACMU		
ID	LEMI_MACMU	
AC	Q95198;	STANDARD;
		PRT; 372 AA

DT	01-NOV-1997 (Rel. 35, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	01-NOV-1997 (Rel. 35, Last annotation update)	
DE	MOLECULE-1) (LAM-1) (LEUKOCYTE-HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE 1)	
DE	(LECAM1) (CD62L).	
GN	SELL.	
OS	Macaca mulatta (Rhesus macaque).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;	
OC	Cercopithecinae; Macaca.	
OX	NCBI_TaxID=9544;	
RA	[1]	
RA	SEQUENCE FROM N.A.	
RA	Budman J.I., Fu H., Johnson C.E., Thakur A.B., Berg E.L.,	
RL	Tsurushita N.;	
CC	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.	
CC	-1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADHERENCE	
CC	OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL	
CC	VENUES IN PERIPHERAL LYMPH NODES.	
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
CC	-1- SIMILARITY: TO OTHER SELECTINS/LECAMs.	
CC	-1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.	
CC	-1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
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CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-slb.ch/announce/	
CC	or send an email to license@isb-slb.ch).	
CC	-----	
DR	EMBL: U73730; AAB18246.1; -	
DR	HSSP: P14151; 1KUD.	
DR	InterPro: IPR000436; -	
DR	InterPro: IPR000561; -	
DR	InterPro: IPR001304; -	
DR	InterPro: IPR002396; -	
DR	Pfam: PF00008; EGF_1.	
DR	Pfam: PF00059; lectin_c_1.	
DR	Pfam: PF00084; sushi_2.	
DR	PRINTS: PR00343; SELECTIN.	
DR	PROSITE: PS00022; EGF_1; 1.	
DR	PROSITE: PS01186; EGF_2; 1.	
DR	PROSITE: PS00615; C-TYPE LECTIN_1; 1.	
DR	PROSITE: PS50041; C-TYPE LECTIN_2; 1.	
KW	Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;	
KW	Selectin; Signal; Sushi; Repeat.	
FT	SIGNAL 1 28	
FT	PROPEP 29 38	
FT	CHAIN 39 372	
FT	DOMAIN 39 332	
FT	TRANSMEM 333 355	
FT	DOMAIN 356 372	
FT	DOMAIN 55 155	
FT	DOMAIN 156 192	
FT	DOMAIN 196 317	
FT	DOMAIN 196 255	
FT	DOMAIN 258 317	
FT	DISULFID 57 155	
FT	DISULFID 128 147	
FT	DISULFID 160 171	
FT	DISULFID 165 180	
FT	DISULFID 182 191	
FT	DISULFID 197 241	
FT	DISULFID 227 254	
FT	DISULFID 259 303	
FT	DISULFID 289 316	
FT	CARBOHYD 60 60	
FT	CARBOHYD 104 104	
FT	CARBOHYD 177 177	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	L-SELECTIN.	
FT	EXTRACELLULAR (POTENTIAL).	
FT	POTENTIAL.	
FT	CYTOPLASMIC (POTENTIAL).	
FT	C-TYPE LECTIN (SHORT FORM).	
FT	EGF-LIKE.	
FT	2 X SUSHI (SCR) REPEATS.	
FT	SUSHI 1.	
FT	SUSHI 2.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).	

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FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 372 AA; 42109 MW; 08BD7DD5AC549D6D CRC64;

Query Match 94.3%; Score 1996; DB 1; Length 372;
Best Local Similarity 93.8%; Pred. No. 1,8e-155;
Matches 349; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

OY 1 MIPPMKQSTQORDLWNIIFKLMGWTMLCCDFLAHHGTCTWYHYSEKPMNQARRFCRDN 60
DB 1 MIPPMKQSTQORDLWNIIFKLMGWTMLCCDFLAHHGTCTWYHYSEKPMNQARRFCRDN 60
OY 61 YTDLVAIQNAEIEYLEKTLPRFSRSYYWIGIRKIGIWTWVGNKSLTEBAENMGDEPN 120
DB 61 YTDLVAIQNAEIEYLEKTLPRFSRSYYWIGIRKIGIWTWVGNKSLTEBAENMGDEPN 120
OY 121 NKKNKEDCVCVEIYIKRNKDAGKNDACCHKAKALCTYASQPMSCSGHGCEVELINNHTC 180
DB 121 NKKNKEDCVCVEIYIKRNKDAGKNDACCHKAKALCTYASQPMSCSGHGCEVELINNHTC 180
OY 181 NCDVGYGPOCOLVIOCEPLAEPLGTMCTHPHGFNFSSQCAFSCSEGTNLGTIEETT 240
DB 181 NCDVGYGPOCOLVIOCEPLAEPLGTMCTHPHGFNFSSQCAFSCSEGTNLGTIEETT 240
OY 241 CGPFGNMSSPEPTCOVYIOCEPLAPDLGIMNCSHPLASFSTACTPFCSEGTLLIGKKK 300
DB 241 CGPFGNMSSPEPTCOVYIOCEPLAPDLGIMNCSHPLASFSTACTPFCSEGTLLIGKKK 300
OY 301 TIESSGIMNSPFIQCKLDKSMIKEGDYNLFIPVAVMTAFSLAIIIMLARLKK 360
DB 301 TIESSGIMNSPFIQCKLDKSMIKEGDYNLFIPVAVMTAFSLAIIIMLARLKK 360
OY 361 GKRSKSMNDPY 372
DB 361 GKRSKSMNDPY 372
OY 361 GKRSKSMNDPY 372
DB 361 GKRSKSMNDPY 372

RESULT 5
LEML_PAPHA STANDARD: PRT: 372 AA.
ID LEML_PAPHA 028768;
AC 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 01-NOV-1997 (rel. 35, Last annotation update)
DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUCOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUCOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).
DE (LECAM1) (CD62L).
GN SELN.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97128794; PubMed=8973334;
RA Tauschita N., Fu H., Berg E.L.;
RT PCR cloning of the cDNA encoding baboon L-selectin."
RL Gene 181:219-220(1996).
CC -1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATES THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL VENULES IN PERIPHERAL LYMPH NODES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U52074; ABA0903.1; -.
DR HSSP: P14151; 1KJB.
DR InterPro: IPR000436; -.
DR InterPro: IPR000561; -.
DR InterPro: IPR001304; -.
DR InterPro: IPR002396; -.
DR Pfam: PF00008; EGF_1.
DR Pfam: PF00059; lectin_C; 1.
DR Pfam: PF00084; sushi; 2.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE LECTIN_2; 1.
DR PROSITE: PS50041; C-TYPE LECTIN_1; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sushi; Repeat.
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 372
FT DOMAIN 39 332
FT TRANSMEM 333 335
FT DOMAIN 356 372
FT DOMAIN 55 155
FT DOMAIN 156 192
FT DOMAIN 196 317
FT DOMAIN 196 255
FT DOMAIN 258 317
FT DISULFID 57 155
FT DISULFID 128 147
FT DISULFID 160 171
FT DISULFID 165 180
FT DISULFID 182 191
FT DISULFID 197 241
FT DISULFID 227 254
FT DISULFID 259 303
FT DISULFID 289 316
FT CARBOHYD 60 60
FT CARBOHYD 104 104
FT CARBOHYD 177 177
FT CARBOHYD 226 226
FT CARBOHYD 232 232
FT CARBOHYD 246 246
FT CARBOHYD 271 271
SQ SEQUENCE 372 AA; 42091 MW; 64E7BDD5AC549D69 CRC64;

Query Match 94.1%; Score 1992; DB 1; Length 372;
Best Local Similarity 93.5%; Pred. No. 3,8e-155;
Matches 348; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

OY 1 MIPPMKQSTQORDLWNIIFKLMGWTMLCCDFLAHHGTCTWYHYSEKPMNQARRFCRDN 60
DB 1 MIPPMKQSTQORDLWNIIFKLMGWTMLCCDFLAHHGTCTWYHYSEKPMNQARRFCRDN 60
OY 61 YTDLVAIQNAEIEYLEKTLPRFSRSYYWIGIRKIGIWTWVGNKSLTEBAENMGDEPN 120
DB 61 YTDLVAIQNAEIEYLEKTLPRFSRSYYWIGIRKIGIWTWVGNKSLTEBAENMGDEPN 120
OY 121 NKKNKEDCVCVEIYIKRNKDAGKNDACCHKAKALCTYASQPMSCSGHGCEVELINNHTC 180
DB 121 NKKNKEDCVCVEIYIKRNKDAGKNDACCHKAKALCTYASQPMSCSGHGCEVELINNHTC 180
OY 181 NCDVGYGPOCOLVIOCEPLAEPLGTMCTHPHGFNFSSQCAFSCSEGTNLGTIEETT 240
DB 181 NCDVGYGPOCOLVIOCEPLAEPLGTMCTHPHGFNFSSQCAFSCSEGTNLGTIEETT 240
OY 241 CGPFGNMSSPEPTCOVYIOCEPLAPDLGIMNCSHPLASFSTACTPFCSEGTLLIGKKK 300
```

FW	Signal	Signal	Sushi	Repeat
FT	PROPEP	1	28	POTENTIAL.
FT	CHAIN	29	38	POTENTIAL.
FT	CHAIN	39	370	L-SELECTIN.
FT	DOMAIN	39	333	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	334	350	POTENTIAL.
FT	DOMAIN	355	370	CYTOPLASMIC (POTENTIAL)
FT	DOMAIN	55	155	C-TYPE LECTIN (SHORT FORM).
FT	DOMAIN	156	192	EGF-LIKE.
FT	DOMAIN	196	317	2 X SUSHI (SCR) REPEATS.
FT	DOMAIN	196	255	SUSHI 1.
FT	DOMAIN	258	317	SUSHI 2.
FT	DISULFID	57	155	BY SIMILARITY.
FT	DISULFID	128	147	BY SIMILARITY.
FT	DISULFID	160	171	BY SIMILARITY.
FT	DISULFID	165	180	BY SIMILARITY.
FT	DISULFID	182	191	BY SIMILARITY.
FT	DISULFID	197	241	BY SIMILARITY.
FT	DISULFID	227	254	BY SIMILARITY.
FT	DISULFID	259	303	BY SIMILARITY.
FT	DISULFID	289	316	BY SIMILARITY.
FT	CARBOHYD	60	60	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	77	77	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	104	104	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	177	177	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	216	216	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	226	226	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	246	246	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	308	308	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	320	320	N-LINKED (GLCNAC. .) (POTENTIAL).
SEQ	SEQUENCE	370 AA;	41971 MW;	92168F816AE9228 CRC64;

Query Match	79.5%;	Score 1682;	DB 1;	Length 370;
Best Local Similarity	77.0%;	Pred. No. 6.5e-130;		
Matches 282;	Conservative 42;	Mismatches 40;	Indels 2;	Gaps 1.
QY 1	MIFPMKQOSTQBDLWNIFFKMGWTLMLCDPLAHGTYGWTYHSEKPMNOMARRECRDN	60		
DB 1	MCPMWCQANORGLMNVFPLMWIMLCCDFPAHGHGDCWTHYHSKRPMPMEKARAFRCRN	60		
QY 61	YVDLVAIQKAAEEYEYKTLFPRSRYWYGIKIGIIMWYGTGNSLTPEANWGDGEPN	120		
DB 61	YVDLVAIQKAAEEYEYKTLFPRSRYWYGIKIGIIMWYGTGNSLTPEANWGDGEPN	120		
QY 121	NKKNKDEVEIYIKRNKDGAKMNDACHKRLKALCYTASQCPMSSGAGCEVEIINNHTC	180		
DB 121	NKRSEKDECEVEIYIKRNKDGSKMNDACHKAKTALCYTASCKPMSSGHQCEVEIINNHTC	180		
QY 181	NCDVGYGGQCCOLVIOCEPLAEPLGMDCHTPFGNFSFSSQACSCSEGNLTGIEETT	240		
DB 181	NCDLGYTGPCCFVYQCVPLPAKLGTMACHPLDGNFMSQCAFNCSKGTDMIGVEETT	240		
QY 241	CGPFGNWSPEPTCCOVIOCEPLASPDGLGIMNCSHPLASFSFQASCTFTSCSTGTELIGKKK	300		
DB 241	CAPFENMSSPEPTCCAVIOCEPLTEPDLGTMOCNHRPLVDGFGSSITCFSCSEBAELTGKKK	300		
QY 301	TTCSSGIGMSNSPFCQCLDKSFSKIGKQDNPFLPYAVNVTAFSGIAFTIIMLARLKK	360		
DB 301	TTCGIGMSNWSPPRCQKINRTISINESDYNPLFPIYAVNVTAFSGIAFTIIMLARLK -	359		
QY 361	GKRSKR 366			
DB 360	RKRSK 364			


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RL Cell 56:1045-1055(1989).
RN [4]
RP SEQUENCE OF 1-360 FROM N.A.
RX MEDLINE-91169529; Pubmed-2004776;
RA Dovenko D.J., Diep A., Taylor B.A., Lusis A.J., Lasky L.A.;
RT "Characterization of the murine homing receptor gene reveals
RT correspondence between protein domains and coding exons.";
RT Genomics 9:270-277(1991).
CC -1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDATE THE ADHERENCE
CC OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
CC VENUES IN PERIPHERAL LYMPH NODES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
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CC -----
DR EMBL: X14772; CAA32880.1; -
DR EMBL: M36005; AAA39722.1; -
DR EMBL: M25324; -; NOT_ANNOTATED_CDS.
DR EMBL: M64549; AA75651.1; -
DR EMBL: M64440; AA75651.1; JOINED.
DR EMBL: M64345; AA75651.1; JOINED.
DR EMBL: M64548; AA75651.1; JOINED.
DR PIR: A33375; A32375.
DR HSSP: P14151; 1KJB.
DR MGD: MGI:98279; Sell.
DR InterPro: IPR000436; -
DR InterPro: IPR000361; -
DR InterPro: IPR001304; -
DR InterPro: IPR002396; -
DR Pfam: PF00008; EGF_1.
DR Pfam: PF00059; lectin_C_1.
DR Pfam: PF00084; sush1_2.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS00615; C-TYPE-LECTIN_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00041; C-TYPE-LECTIN_2; 1.
DR Cell adhesion: Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sush1; Repeat.
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 372
FT DOMAIN 39 332
FT TRANSMEM 333 355
FT DOMAIN 356 372
FT DOMAIN 55 155
FT DOMAIN 156 192
FT DOMAIN 196 317
FT DOMAIN 317 255
FT DOMAIN 258 317
FT DISULFID 57 155
FT DISULFID 128 147
FT DISULFID 160 171
FT DISULFID 165 180
FT DISULFID 182 191
FT DISULFID 197 241
FT DISULFID 227 254
FT DISULFID 259 303
FT DISULFID 289 316
FT CARBOHYD 60 104
FT CARBOHYD 104 177
FT CARBOHYD 177 177

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FT CARBOHYD 216 216 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CONFLICT 32 32 I -> T (IN REF. 4).
SQ SEQUENCE 372 AA; 42288 MW; 4433EDF64CB2B78 CRC64;

Query Match 78.0%; Score 1651; DB 1; Length 372;
Best Local Similarity 76.1%; Pred. No. 2,2e-127;
Matches 283; Conservative 32; Mismatches 57; Indels 0; Gaps 0;

QY 1 MPPMKCOSTORDLWNIIFKLGWTLICDPLAHGHGYCTWYHYSEKPMNMOARRECDN 60
D 1 MPPMKCEGTWGSRNILKLTWTLICDPLHGHGHCTHYSEKPMNWEARKEFCQN 60
/ 61 YTDVLAIONKAELEYELKLPFSRSTYWGIRKIGIWTWGTNKSLTDEAENMGDEPN 120
D 61 YTDVLAIONKRELEYELNTLPSPYYWIGIRKIGKMTWGTNKTLYKEAENMGAGEPN 120
QY 121 NKKNKEDVEIYIKRKDGKWNDDACHKKAALCYTASCOFMSGSGHEVEITNNHTC 180
D 121 NKKSKEDVEIYIKRKRDGKWNDDACHKKAALCYTASCOFSGNGKEVEITNNHTC 180
QY 181 NCDVGYGPCCOLVIOCEPLEAPELGTMDCIHPFNFSFSCAFSCSEGTNLGIEETT 240
D 181 IDGAGYGPCCQVVOCEPLEAPELGTMDCIHPFNFSFSCAFSCSEGTNLGIEETT 240
QY 241 CGPFGWSSPEPTCOVIOCEPLSAPDLGIMNSHPLASFPSACTFICSGTELGK 300
D 241 CGASGWSPEPTCOVVOCEPLEAPELGTMDCIHPFNFSFSCAFSCSEGTNLGIEETT 300
QY 301 TICESGIMNSNPICOKLIDKFSMIKEGDYNPLEPIPAVWVTFSGLAFTIWLARL 360
D 301 TCGASGWSPEPTCOVVOCEPLEAPELGTMDCIHPFNFSFSCAFSCSEGTNLGIEETT 360
QY 361 GKSKRSNDPY 372
D 361 GKSKRSNDPY 372
DB 361 GKSKRSNDPY 372

RESULT 9
LEMS_SHEEP STANDARD; PRT; 769 AA.
ID LEMS_SHEEP
AC P98109;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
DE (CD62P) (LEUCOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
GN SELP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprine; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Burns S.A., Neufeld E.J., Donady J.J.;
RT Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
CC INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC LEUCOCYTES. THE LIGAND RECOGNIZED IS SIALLYL-LEWIS X.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.

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RN      [4]
RP      3D-STRUCTURE MODELLING OF 42-161.
RX      MEDLINE=94033388; PubMed=7505860;
RA      Bajorath J., Stenkamp R., Aruffo A.;
RT      "Knowledge-based model building of proteins: concepts and examples.";
RL      Protein Sci. 2:1798-1810(1993).
RN      [5]
RP      VARIANTS ASN-331; ASP-603; VAL-640 AND PRO-756.
RX      MEDLINE=98334547; PubMed=9668170;
RA      Herrmann S.M., Ricard S., Nicaud V., Mallet C., Evans A.,
RT      Ruidavets J.B., Arveiler D., Luc G., Cambien F.;
RT      "The P-selectin gene is highly polymorphic: reduced frequency of the
RT      Pro151 allele carriers in patients with myocardial infarction.";
RL      Hum. Mol. Genet. 7:1277-1284(1998).
CC      -1- FUNCTION: CA12(+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC      TO CARBOHYDRATES ON NETROPHILS AND MONOCYTES. MEDIATES THE
CC      INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC      LEUCOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
CC      AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
CC      ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
CC      THE CELL SURFACE.
CC      -1- SIMILARITY: TO OTHER SELECTINS/LECAMS.
CC      -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC      -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC      -1- SIMILARITY: CONTAINS 9 SUSHI (SCR) REPEATS.
CC      -1- DATABASE: NAME=PROW; NOTE=CD guide CD62p entry;
CC      WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd62p.htm".
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL, M60234; AAA35910.1; JOINED.
DR      EMBL, M60217; AAA35910.1; JOINED.
DR      EMBL, M60218; AAA35910.1; JOINED.
DR      EMBL, M60219; AAA35910.1; JOINED.
DR      EMBL, M60222; AAA35910.1; JOINED.
DR      EMBL, M60223; AAA35910.1; JOINED.
DR      EMBL, M60224; AAA35910.1; JOINED.
DR      EMBL, M60225; AAA35910.1; JOINED.
DR      EMBL, M60226; AAA35910.1; JOINED.
DR      EMBL, M60227; AAA35910.1; JOINED.
DR      EMBL, M60228; AAA35910.1; JOINED.
DR      EMBL, M60229; AAA35910.1; JOINED.
DR      EMBL, M60231; AAA35910.1; JOINED.
DR      EMBL, M60232; AAA35910.1; JOINED.
DR      EMBL, M60233; AAA35910.1; JOINED.
DR      EMBL, M25322; -, NOT_ANNOTATED_CDS.
DR      PIR, A30359; A30359.
DR      PDB, 1FSB; 01-APR-97.
DR      PDB, 1KUD; 03-APR-96.
DR      MIM, 173610; -.
DR      InterPro; IPR000436; -.
DR      InterPro; IPR000561; -.
DR      InterPro; IPR001304; -.
DR      InterPro; IPR002396; -.
DR      Pfam; PF00008; EGF_1.
DR      Pfam; PF00059; lectin_C; 1.
DR      Pfam; PF00084; sushi; 9.
DR      PRINTS; PR00343; SELECTIN.
DR      PROSITE; PS00022; EGF_1; 1.
DR      PROSITE; PS01186; EGF_2; 1.
DR      PROSITE; PS00615; C-TYPE_LLECTIN_2; 1.
DR      PROSITE; PS50041; C-TYPE_LLECTIN_2; 1.
DR      Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
DR      Selectin; Signal; Sushi; Repeat; Lipoprotein; Palmitate; Polymorphism;
KW      3D-structure.

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FT	SIGNAL	1	41	830	P-SELECTIN, EXTRACELLULAR (POTENTIAL), POTENTIAL.
FT	CHAIN	42	771	795	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	772	795	830	C-TYPE LECTIN (SHORT FORM), EGF-LIKE.
FT	TRANSHEM	796	830	158	9 X SUSHI (SCR) REPEATS.
FT	DOMAIN	159	195	199	SUSHI 1.
FT	DOMAIN	199	258	320	SUSHI 2.
FT	DOMAIN	261	320	382	SUSHI 3.
FT	DOMAIN	323	382	444	SUSHI 4.
FT	DOMAIN	385	444	506	SUSHI 5.
FT	DOMAIN	447	506	568	SUSHI 6.
FT	DOMAIN	509	568	571	SUSHI 7.
FT	DOMAIN	571	630	700	SUSHI 8.
FT	DOMAIN	641	700	762	SUSHI 9.
FT	DOMAIN	703	762	158	BY SIMILARITY.
FT	DISULFID	60	158	150	BY SIMILARITY.
FT	DISULFID	131	150	174	BY SIMILARITY.
FT	DISULFID	163	183	194	BY SIMILARITY.
FT	DISULFID	168	183	244	BY SIMILARITY.
FT	DISULFID	185	194	257	BY SIMILARITY.
FT	DISULFID	200	244	306	BY SIMILARITY.
FT	DISULFID	230	257	319	BY SIMILARITY.
FT	DISULFID	262	306	381	BY SIMILARITY.
FT	DISULFID	292	319	430	BY SIMILARITY.
FT	DISULFID	324	368	443	BY SIMILARITY.
FT	DISULFID	354	381	492	BY SIMILARITY.
FT	DISULFID	385	430	505	BY SIMILARITY.
FT	DISULFID	416	443	554	BY SIMILARITY.
FT	DISULFID	448	492	567	BY SIMILARITY.
FT	DISULFID	478	505	629	BY SIMILARITY.
FT	DISULFID	510	554	672	BY SIMILARITY.
FT	DISULFID	540	567	704	BY SIMILARITY.
FT	DISULFID	572	616	734	BY SIMILARITY.
FT	DISULFID	602	629	761	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	642	666	98	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	672	699	98	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	704	748	180	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	734	761	212	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	54	54	219	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	98	98	411	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	180	180	460	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	212	212	518	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	219	219	665	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	411	411	716	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	460	460	723	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	518	518	807	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	565	665	821	ENDOCYTOSIS SIGNAL (PROBABLE).
FT	CARBOHYD	665	665	311	S. -> N.
FT	LIPID	807	807	603	N-> D.
FT	SITE	818	821	640	/FTID=VAR_004192.
FT	VARIANT	311	311	756	N-> V.
FT	VARIANT	603	603	756	/FTID=VAR_004194.
FT	VARIANT	640	640		T -> P (REDUCED FREQUENCY IN PATIENTS WITH MYOCARDIAL INFARCTION).
FT	VARIANT	756	756		/FTID=VAR_004195.
FT	SEQUENCE	830 AA;	90844 MM;		FBC407BA2579F6EB CRC64;
FT	Query Match	42.8%;	Score 905;	DB 1;	Length 830;
FT	Best Local Similarity	50.6%;	Pred. No. 2,9e-66;		
FT	Matches 157;	Conservative 47;	Mismatches 106;	Indels 0;	Gaps 0;
DB	8	OSTOGLDLMNIFKLMGWTMLCCDFLAHGHGTCYCTHYSEKPMWQARRECRDNYDLVAI	67		
DB	11	ORFGQVVGISGLLCSFSLISELTGKQEKVAMTYSYRKASVMNISRKYCCQNRYYDLVAI	70		


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OY 68 QNKAETIYLEKTIPEFSNYYWIGRTGRTWYGTNKSLETEENNGDEPNKKKKED 127
DB 71 QNNNEIDYLNKVVYSSYYWIGIRKNNKNTWGTGRTKALTNEANMADENPNKKRNNED 130
OY 128 CVELIYIRKNDACKGNDACDKHLKALCYTASCOVSCSGHECEVELINNHTCNCDVGY 187
DB 131 CVELIYIRKNDACKGNDACDKHLKALCYTASCOVSCSGHECEVELINNHTCNCDVGY 190
OY 188 GPOCQVLYOCEPLEAPBLGMDCTHPPGNFSFSCAFSCSEGTNLGIEETTCGPGN 247
DB 191 GPCEYVRECGEELDPGVHVMNCNSHPNGNSFCFCTDGYQVNGPSEKLECLAGIM 250
OY 248 SSEPPTQVYQCEPLAPDLGJNCSHPLASFSTACTICSTGLKGGKKTICSSG 307
DB 251 TNNPPOCLAQQCPPLKIPERGMNMLCHSAKAFHQSSCSFCEGFGALVPEVVOCTASG 310
OY 308 TMSNPSPICQ 317
DB 311 VMTAPAPVCK 320

RESULT 11
LEW3 MOUSE STANDARD; PRT: 768 AA.
AC Q01102;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (PADGEM)
DE (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
GN SELP OR GRMP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92340571; PubMed=1378846;
RA Weller A., Isenmann S., Vestweber D.;
RT "Cloning of the mouse endothelial selectins. Expression of both E-
RT and P-selectin is inducible by tumor necrosis factor alpha.";
RL J. Biol. Chem. 267:15176-15183(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=92345617; PubMed=1379089;
RA Sanders W.E., Jr., Wilson R.W., Ballantyne C.M., Beaudet A.L.;
RT "Molecular cloning and analysis of in vivo expression of murine P-
RT selectin.";
RL Blood 80:795-800(1992).
CC -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
CC INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
CC AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
CC ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
CC THE CELL SURFACE.
CC -1- INDUCTION: BY TUMOR NECROSIS FACTOR ALPHA.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; MOUSE P-LECTIN LACKS
CC THE HUMAN SUSHI-2 EQUIVALENT.
CC -----
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CC or send an email to license@isb-sib.ch).
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CC -----
CC EMBL: M87861; AAA40008.1; -.
CC EMBL: M72332; AAA37712.1; -.
CC PIR: A42755; A42755.
CC HSSP: P16109; 1FSB.
CC MGD: MGI:98280; Selp.
CC InterPro: IPR000436; -.
CC InterPro: IPR000561; -.
CC InterPro: IPR001304; -.
CC InterPro: IPR002396; -.
CC Pfam: PF00008; EGF_1.
CC Pfam: PF00059; lectin_C; 1.
CC Pfam: PF00084; sushi; 8.
CC PRINTS: PR00343; SELECTIN.
CC PROSITE: PS00022; EGF_1; 1.
CC PROSITE: PS0186; EGF_2; 1.
CC PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
CC PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
CC Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
CC Selectin; Signal; Sushi; Repeat; Lipoprotein; Palmitate.
CC SIGNAL 1 41
CC CHAIN 42 768
CC DOMAIN 42 709
CC TRANSMEM 710 733
CC DOMAIN 734 768
CC DOMAIN 58 158
CC DOMAIN 159 195
CC DOMAIN 199 700
CC DOMAIN 199 258
CC DOMAIN 261 320
CC DOMAIN 323 382
CC DOMAIN 385 444
CC DOMAIN 447 506
CC DOMAIN 509 568
CC DOMAIN 579 638
CC DOMAIN 641 700
CC DISULFID 60 158
CC DISULFID 131 150
CC DISULFID 163 174
CC DISULFID 168 183
CC DISULFID 185 194
CC DISULFID 200 244
CC DISULFID 230 257
CC DISULFID 262 306
CC DISULFID 292 319
CC DISULFID 324 368
CC DISULFID 354 381
CC DISULFID 386 430
CC DISULFID 416 443
CC DISULFID 448 492
CC DISULFID 478 505
CC DISULFID 510 554
CC DISULFID 540 567
CC DISULFID 580 624
CC DISULFID 610 637
CC DISULFID 642 686
CC DISULFID 672 699
CC CARBOHYD 398 398
CC CARBOHYD 603 603
CC CARBOHYD 654 654
CC CARBOHYD 661 661
CC CARBOHYD 679 679
CC LIPID 745 745
CC SITE 756 759
CC CONFLICT 724 724
CC SEQUENCE 768 AA; 83098 MW; E5173074D2F66E8 CRC64;

Query Match 42.7%; Score 902.5; DB 1; Length 768;
Best Local Similarity 52.0%; Pred. No. 4.3e-66;
Matches 156; Conservative 40; Mismatches 103; Indels 1; Gaps 1;
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OY 20 LMGWTMLCCPFLAHNGYVCWYHSEKPMQWRARRCRONVTDVAIQNKAETIYLEKTI 79
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Db 24 IW-FSALISELVNOKEVAAATYNTYSTRKAYSWMNSRVCRRHFTDVALIONKNEIAHLNDV 82
QY 80 LPEFSRYWIGIRKIGITWTWGTNKLTEPEANNDGDGPNKKKKKECEVEIYIRKMDA 139
Db 83 IPEFNSYWIGIRKINNKWTWGTNKLTEPEANNDGPNKKKKKECEVEIYIRKMDA 142
QY 140 GWRNDACKKLAAALCYTASCPMCSGHECEVEIINNHTCNDVGYXPOCOLVIOCEP 199
Db 143 GWRNDPECKRRRACLYTASCPMCSGHECEVEIINNHTCNDVGYXPOCOLVIOCEP 202
QY 200 LEAPELGTMDCTHPPGNSFSSSCAFSCSEGNLTGIEETCGPPGNSSPEPTCOVIQC 259
Db 203 VAIRPHVLMNCHPLGEFSSNSQCTFSCAEGVELDPELOCLASGIVTNNPPKDAVQC 262
QY 260 EPLASPDGIMNCHPLASFSFTACTPFCSEGTLEICKKTKICESGIGWNSPPIQOKL 319
Db 263 QSLAPPGHTMACMHPAIAFAYDSSCKRECQPGYRARSNTLHCTGSGQWSEPLPTCEAI 322

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RESULT 12

LEM3_BOVIN STANDARD; PRT; 646 AA.

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ID LEM3_BOVIN STANDARD; PRT; 646 AA.
AC P42201;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
DE (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
GN SELP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Capillary endothelium;
RX MEDLINE=93249394; Pubmed=7683458;
RA Strubel N.A., Nguyen M., Kansas G.S., Tedder T.F., Bischoff J.;
RT "Isolation and characterization of a bovine cdna encoding a
RT functional homolog of human P-selectin."
RL Biochem. Biophys. Res. Commun. 192:338-344(1993).
CC -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
CC INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
CC AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
CC ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
CC THE CELL SURFACE.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS; BOVINE P-LECTIN LACKS
CC THE HUMAN SUSHI-3, -4 AND -7 EQUIVALENTS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U12041; AAA30743.1; -
DR HSP: P16109; 15SB.
DR InterPro: IPR000436; -
DR InterPro: IPR000561; -
DR InterPro: IPR001304; -
DR InterPro: IPR002396; -
DR Pfam: PF00008; EGF_1.

```

```

DR Pfam: PF00059; lectin_c; 1.
DR Pfam: PF00084; sushi; 6.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS0186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sushi; Repeat.
FT SIGNAL 1 41
FT CHAIN 42 646
FT DOMAIN 42 587
FT TRANSMEM 588 611
FT DOMAIN 612 646
FT DOMAIN 38 158
FT DOMAIN 159 195
FT DOMAIN 199 578
FT DOMAIN 199 258
FT DOMAIN 261 320
FT DOMAIN 323 382
FT DOMAIN 385 444
FT DOMAIN 457 516
FT DOMAIN 519 578
FT DISULFID 60 158
FT DISULFID 131 150
FT DISULFID 163 174
FT DISULFID 168 183
FT DISULFID 185 194
FT DISULFID 200 244
FT DISULFID 230 257
FT DISULFID 262 306
FT DISULFID 292 319
FT DISULFID 324 368
FT DISULFID 354 381
FT DISULFID 386 430
FT DISULFID 416 443
FT DISULFID 458 502
FT DISULFID 488 515
FT DISULFID 520 564
FT DISULFID 550 577
FT CARBOHYD 48 48
FT CARBOHYD 54 54
FT CARBOHYD 80 80
FT CARBOHYD 180 180
FT CARBOHYD 212 212
FT CARBOHYD 219 219
FT CARBOHYD 336 336
FT CARBOHYD 481 481
FT CARBOHYD 532 532
FT CARBOHYD 539 539
FT CARBOHYD 557 557
FT SITE 634 637
SQ SEQUENCE 646 AA; 71229 MW; 573912A4627A6ACA CRC64;

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Query Match 42.3%; Score 894.5; DB 1; Length 646;
 Best Local Similarity 48.7%; Pred. No. 1.6e-65;
 Matches 155; Conservative 51; Mismatches 109; Indels 3; Gaps 1;

```

QY 2 IFPKCOSTRODLAMNFKLMGWTMLCCDFLAHGYTCWYHSEKPMKQRRRCRQNY 61
Db 8 IMMNR---TQRAVFRVQLCTSVLFEVINOKEVSAMWYHNSNTYSMNYSRAFCQRY 64
QY 62 TDVAIONKAEIYELEKTLPEFSRSYWIGIRKIGIWTWGTNKSILTEBAEWGDEPN 121
Db 65 TDVAIONKNEIAYLNETLIPYNSYWIGIRKINNKWTWGTNKLTEBAENADNEPN 124
QY 122 KKKKECEVEIYIRKMDACKWADACKKLAAALCYTASCPMCSGHECEVEIINNHTCN 181
Db 125 KRNNDCEVEIYIKTSAPKNDDECKRRKRALCYRASCODMSCSKQCEIETIGNYCS 184
QY 182 CDVGYGPOCOLVIOCEPLAEPLGTMDCTHPPGNSFSSSCAFSCSGTNLTGIEETC 241

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Db 185 CYPFGVGECEYRECEFDLPQHVMNCSPHPLGNFNSHCSPHCAGYALNPSLEEC 244
QY 242 GPPGNMSSPEPTQVIOCEPLSLAPDLGINMCSHPLASFSSTACTFICSECTELIGKKKT 301
Db 245 LAGIMWTNSPPQCAVAVOCFPAKSPQSGMSCVQSAEAFQHSQSCSFCEGFGALVGEV 304
QY 302 ICSSGIMWSNPICOKL 319
Db 305 HCTALGWTAPTPVCKAL 322

RESULT 13
LEMS RAT
ID LEMS RAT STANDARD; PRT; 768 AA.
AC P98106;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
DE (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
GN SELP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA MEDLINE=94333817; PubMed=7520013;
RA Auchampach J.A., Oliver M.G., Anderson D.C., Manning A.M.;
RT "Cloning, sequence comparison and in vivo expression of the gene
RT encoding rat P-selectin.";
RL Gene 145:251-255(1994).
CC -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
CC INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED: SPLEEN,
CC LUNG, BRAIN, LIVER, HEART, KIDNEY, THYMUS, SMALL INTESTINE.
CC -1- INDUCTION: ACUTE INFLAMMATION (PROBABLY).
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; RAT P-LECTIN LACKS THE
CC HUMAN SUSHI-2 EQUIVALENT.
CC -----
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CC -----
CC EMBL, L23088; AAA60325.1; --
DR HSSP; P16109; IFSB.
DR InterPro; IPR000436; --
DR InterPro; IPR000561; --
DR InterPro; IPR001396; --
DR InterPro; IPR002396; --
DR Pfam; PF00059; Lectin_C; 1.
DR Pfam; PF00084; sush1; 8.
DR PRINTS; PR00343; SELECTIN.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE; PS00615; C-TYPE_LECTIN_2; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sushi; Repeat; Lipoprotein; Palmitate.
FT SIGNAL 1 41
FT CHAIN 42 768
FT DOMAIN 42 709
EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 710 733
FT DOMAIN 734 768
FT DOMAIN 38 158
FT DOMAIN 159 195
FT DOMAIN 199 700
FT DOMAIN 199 258
FT DOMAIN 261 320
FT DOMAIN 323 382
FT DOMAIN 385 444
FT DOMAIN 447 506
FT DOMAIN 509 568
FT DOMAIN 579 638
FT DOMAIN 641 700
FT DISULEID 60 158
FT DISULEID 131 150
FT DISULEID 168 183
FT DISULEID 185 194
FT DISULEID 200 244
FT DISULEID 230 257
FT DISULEID 262 306
FT DISULEID 292 319
FT DISULEID 324 368
FT DISULEID 354 381
FT DISULEID 386 430
FT DISULEID 416 443
FT DISULEID 448 492
FT DISULEID 478 505
FT DISULEID 510 554
FT DISULEID 540 567
FT DISULEID 580 624
FT DISULEID 610 637
FT DISULEID 642 686
FT DISULEID 672 699
FT CARBOHYD 45 45
FT CARBOHYD 54 54
FT CARBOHYD 107 107
FT CARBOHYD 212 212
FT CARBOHYD 347 347
FT CARBOHYD 456 456
FT CARBOHYD 603 603
FT CARBOHYD 654 654
FT CARBOHYD 661 661
FT CARBOHYD 679 679
FT LIPID 745 745
FT SITE 756 759
FT SEQUENCE 768 AA; 83517 MW; 26FD7E8A5F3F1316 CRC64;
SQ

Query Match 41.8%; Score 885; DB 1; Length 768;
Best Local Similarity 53.4%; Pred. No. 1,1e-64;
Matches 150; Conservative 42; Mismatches 89; Indels 0; Gaps 0;
QY 39 WTYISEKPMQARRECRDNYDLVAIONKRIEYLEKTLPPSRASYWIGIRKIGIW 98
Db 42 WTYISKRAKYSMNSRAFCRKHFTDLVAIONKRIALHNDVIPIVNSYTWIGIRKINKW 101
QY 99 TWGVTNKSLEAEENWGDGEPNNKKNKEDCEIYIKRNKQAGKWNDDACHRLKALCYTA 158
Db 102 TWGVTNKTTLAEAEENWADNEPNKRNQDCVEIYIKNSAPAGKWNDDPCFRKRALCYTA 161
QY 159 SCQPMSCSGHGEVEIITNNHNCNDVGTYGQOCLVYIOCEPLEAPBELCTHNCITPFGNFS 218
Db 162 SCQPMSCNSQGERIETIGSYTSCYPCFYEGECYVQECGFIDIPQHYLMNCSPHLDGFS 221
QY 219 FSSQCAFSCSGTNLTGTEETGCPFGMWSPEPTQVIOCEPLSAPDLGIMNCSPHPLAS 278
Db 222 FSSQCTTSCPEGYDNLGNPSEMQCLASGIWTNPPQCAVAVOCQSLAPLHGTMDCTHPLAA 281
QY 279 FSEFTSACTFICSECTELIGKKKTICSSGIWSNPICOKL 319
Db 282 FAYDSSCKFEQPGYRMRGSDILHCTDSQGMSEPLPCEAL 322

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RESULT 14
LEM2_HUMAN STANDARD: PRT: 610 AA.
AC P16581; P16111.
DT 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
DE (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2)
DE (CD62E).
GN SELE OR ELAM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90175359; PubMed=1689848;
RA Hession C., Osborn L., Goff D., Chi-Rosso G., Vassallo C.,
RA Pasek M., Pittack C., Tizard R., Goelz S., McCarthy K., Hopple S.,
RA Lobb R.;
RT "endothelial leukocyte adhesion molecule 1: direct expression cloning
RT and functional interactions.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:1673-1677(1990).
RP SEQUENCE FROM N.A.
RX MEDLINE=89162047; PubMed=2466335;
RA Bevilacqua M.P., Stengelin S., Gimbrone M.A. Jr., Seed B.;
RT "endothelial leukocyte adhesion molecule 1: an inducible receptor for
RT neutrophils related to complement regulatory proteins and lectins.";
RL Science 243:1160-1165(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91115870; PubMed=1703529;
RA Collins T., Williams A., Johnston G.I., Kim J., Eddy R., Shows T.,
RA Gimbrone M.A. Jr., Bevilacqua M.P.;
RT "Structure and chromosomal location of the gene for endothelial-
RT leukocyte adhesion molecule 1.";
RL J. Biol. Chem. 266:2466-2473(1991).
RN [4]
RP LIGAND.
RX MEDLINE=91068005; PubMed=1701274;
RA Phillips M.L., Nudelmann E., Gaeta F.C., Perez M., Singhal A.K.,
RA Hakomori S., Paulson J.C.;
RT "ELAM-1 mediates cell adhesion by recognition of a carbohydrate
RT ligand, sialyl-Lex.";
RL Science 250:1130-1132(1990).
RN [5]
RP 3D-STRUCTURE MODELING OF LECTIN DOMAIN.
RX MEDLINE=93202275; PubMed=7681016;
RA Mills A.;
RT "Modelling the carbohydrate recognition domain of human E-selectin.";
RL FEBS Lett. 319:5-11(1993).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 22-178.
RX MEDLINE=94150646; PubMed=7509040;
RA Graves B.J., Crowther R.L., Chandran C., Rumberger J.M., Li S.,
RA Huang K.-S., Precky D.H., Familletti P.C., Wollitzky B.A., Burns D.K.;
RT "Insight into E-selectin/ligand interaction from the crystal
RT structure and mutagenesis of the lec/EGF domains.";
RL Nature 367:533-538(1994).
RN [7]
RP VARIANT ARG-149.
RX MEDLINE=95179107; PubMed=7533025;
RA Wenzel K., Felix S., Kleber F.X., Brachold R., Menke T., Schatke S.,
RA Schulte K.L., Glaser C., Rohde K., Baumann G., Speer A.;
RT "E-selectin polymorphism and atherosclerosis: an association study.";
RL Hum. Mol. Genet. 3:1935-1937(1994).
RN [8]
RP VARIANT ARG-149.
RX MEDLINE=99134508; PubMed=9933738;
RA Ye S.Q., Usher D., Virgil D., Zhang L.Q., Yochim S.E., Gupta R.;
RT "A pscl polymorphism detects the mutation of serine-128 to arginine in

```

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RT CD 62E gene - a risk factor for coronary artery disease.";
RL J. Biomed. Sci. 6:18-21(1999).
CC -1- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND
CC MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED BY
CC ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES OF
CC POLYACETOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
CC GLYCOLIPIDS).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- POLYMORPHISM: A POLYMORPHISM IN POSITION 149 IS ASSOCIATED WITH A
CC HIGHER RISK OF CORONARY ARTERY DISEASE (CAD). A SIGNIFICANTLY
CC HIGHER MUTATION FREQUENCY (ARG-149) IS OBSERVED IN PATIENTS WITH
CC ANGIOGRAPHICALLY PROVEN SEVERE ATHEROSCLEROSIS COMPARED WITH AN
CC UNSELECTED POPULATION (SER-149).
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD62e entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd62e.htm".
CC -----
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CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL; M30640; AAA52377.1; -
DR EMBL; M61893; AAA52375.1; JOINED.
DR EMBL; M61895; AAA52375.1; JOINED.
DR EMBL; M61887; AAA52375.1; JOINED.
DR EMBL; M61888; AAA52375.1; JOINED.
DR EMBL; M61890; AAA52375.1; JOINED.
DR EMBL; M61891; AAA52375.1; JOINED.
DR EMBL; M61892; AAA52375.1; JOINED.
DR EMBL; M24736; AAA52376.1; -
DR PIR; A32606; A32606.
DR PIR; A35046; A35046.
DR PIR; A38615; A38615.
DR PDB; 1E5L; 31-AUG-94.
DR PDB; 1KJA; 03-APR-96.
DR MIM; 131210; -
DR InterPro; IPR000436; -
DR InterPro; IPR000561; -
DR InterPro; IPR001304; -
DR InterPro; IPR002396; -
DR Pfam; PF00008; EGF_1.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF00084; sushi; 6.
DR PRINTS; PR00343; SELECTIN.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sushi; Repeat; Polymorphism; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 610
FT DOMAIN 22 556
FT TRANSMEM 557 578
FT DOMAIN 579 610
FT DOMAIN 38 138
FT DOMAIN 139 175
FT DOMAIN 179 548
FT DOMAIN 179 238
FT DOMAIN 241 300
FT DOMAIN 303 363
FT DOMAIN 366 426
FT DOMAIN 429 489
FT DOMAIN 492 548
FT DISULFID 40 138
FT 111 130

```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2001, 02:55:12 ; Search time 85 Seconds
(without alignments)
579.029 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116

Sequence: 1 MIFPMKCOSTGRDLMNIFKL.....MLARRLKKGKSKSMNDPY 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP:REMBL.16:*
2: SP:archaea:*
3: SP:bacteria:*
4: SP:fungi:*
5: SP:human:*
6: SP_invertebrate:*
7: SP_mhc:*
8: SP_mhc:*
9: SP_mhc:*
10: SP_mhc:*
11: SP_mhc:*
12: SP_mhc:*
13: SP_mhc:*
14: SP_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2090	98.8	385	09UJ43	09UJ43 homo sapien
2	1796	84.9	376	028629	028629 oryctolagus
3	1667	78.8	372	063762	063762 rattus norv
4	911	43.1	616	095509	095509 homo sapien
5	909	43.0	740	095507	095507 homo sapien
6	898	42.4	740	095508	095508 homo sapien
7	884	41.8	754	028290	028290 mus musculu
8	876.5	41.4	646	028097	028097 sus scrofa
9	860.5	40.7	649	028657	028657 oryctolagus
10	860	40.6	609	09GLFO	09GLFO canis faml
11	815.5	38.5	482	028982	028982 sus scrofa
12	248.5	11.7	3567	09ES77	09ES77 mus musculu
13	247.5	11.7	1124	09YVR4	09YVR4 drosophila
14	237.5	11.2	974	09YVR4	09YVR4 drosophila
15	236	11.2	868	018849	018849 caenorhabd
16	199.5	10.2	1061	09VXX7	09VXX7 drosophila
17	199.5	9.4	449	014570	014570 homo sapien
18	199.5	9.4	449	09NU86	09NU86 homo sapien
19	199.5	9.4	1172	09NU87	09NU87 homo sapien

ALIGNMENTS

20	195	9.2	866	5	0917E3	0917E3 drosophila
21	195	9.2	933	5	0917E4	0917E4 drosophila
22	195	9.2	958	5	09V560	09V560 drosophila
23	192.5	9.1	481	4	09H284	09H284 homo sapien
24	189.5	9.0	1083	5	026423	026423 carcinoscor
25	183	8.6	328	4	09U771	09U771 homo sapien
26	176	8.3	378	6	062837	062837 saguinus oe
27	175.5	8.3	2014	6	029530	029530 pan troglod
28	173	8.2	1653	5	09VIT9	09VIT9 drosophila
29	172	8.1	2039	4	016745	016745 homo sapien
30	172	8.1	2489	4	016744	016744 homo sapien
31	171.5	8.1	395	14	09J2M6	09J2M6 macaca mula
32	171	8.1	354	5	09U611	09U611 drosophila
33	171	8.1	359	5	09V0X3	09V0X3 drosophila
34	170	8.0	314	6	062835	062835 saguinus oe
35	170	8.0	404	4	09NNX6	09NNX6 homo sapien
36	169.5	8.0	559	4	09UQV2	09UQV2 homo sapien
37	168	7.9	292	4	014538	014538 homo sapien
38	168	7.9	533	11	008569	008569 cavia porce
39	166	7.8	1911	6	029528	029528 papio hamad
40	165.5	7.8	560	5	022328	022328 caenorhabd
41	165.5	7.8	1479	11	064449	064449 mus musculu
42	165	7.8	287	4	003969	003969 homo sapien
43	165	7.8	292	4	000448	000448 homo sapien
44	164.5	7.8	377	6	062838	062838 saguinus oe
45	164	7.8	214	11	09R0Q8	09R0Q8 mus musculu

RESULT 1	09UJ43	PRELIMINARY;	PRT;	385 AA.
ID	09UJ43;			
AC	09UJ43;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	L-SELECTIN PRECURSOR.			
GN	L-SELECTIN.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=HEMATOPOIETIC (B LYMPHOCTE);			
RA	Fleiger C.B.;			
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=HEMATOPOIETIC (B LYMPHOCTE);			
RA	Fleiger C.B.;			
RL	Thesis (1998), Freie Universitaet Berlin, Fachbereich Chemie.			
DR	EMBL: AJ246000; CAB5486.1; -.			
DR	HSSP: P14151; IKCB.			
DR	InterPro: IPR000436; -.			
DR	InterPro: IPR000561; -.			
DR	InterPro: IPR001304; -.			
DR	InterPro: IPR002396; -.			
DR	Pfam: PR00008; EGF_1.			
DR	Pfam: PR00059; EGF_1.			
DR	Pfam: PR00084; sushi; 2.			
DR	PRINTS: PR00343; SELECTIN.			
DR	PROSITE: PS00615; C-TYPE_LLECTIN_1; 1.			
DR	PROSITE: PS00615; C-TYPE_LLECTIN_2; 1.			
DR	PROSITE: PS00022; EGF_1; UNKNOWN_1.			
DR	PROSITE: PS01186; EGF_2; 1.			
DR	SMART: SM00032; CCP; 1.			
DR	EGF-like domain; Glycoprotein; Lectin; Selectin; Signal.			
FT	SGNLT			
FT	POTENTIAL.			
FT	CHAIN			
FT	SEQUENCE			

Query Match 98.8%; Score 2090; DB 4; Length 385;
Best Local Similarity 98.9%; Pred. No. 1.6e-197;
Matches 368; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIFPMKCSOTRDLMNFKLMGWTMLCCDFLAHGTGCTYHYSEKPMNORARPCRDN 60
DB 14 MIFPMKCSOTRDLMNFKLMGWTMLCCDFLAHGTGCTYHYSEKPMNORARPCRDN 73
QY 61 YTDVAIONKAEIYELEKTLPFSSRYWIGIRKIGIMTWGNTKSLTEAENMGDEPN 120
DB 74 YTDVAIONKAEIYELEKTLPFSSRYWIGIRKIGIMTWGNTKSLTEAENMGDEPN 133
QY 121 NKKKEDCEVEIYIKRNKDAGKNDACHKLKAALCTYASCPMCSGHECEVEIINNHTC 180
DB 134 NKKKEDCEVEIYIKRNKDAGKNDACHKLKAALCTYASCPMCSGHECEVEIINNHTC 193
QY 181 NCDVGYGPOCQVIOCEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLGIEET 240
DB 194 NCDVGYGPOCQVIOCEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLGIEET 253
QY 241 CGPFGMWSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTACTPTGSEGTLLGKKK 300
DB 254 CGPFGMWSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTACTPTGSEGTLLGKKK 313
QY 301 TIGESSGIMSNPSPIQCKLDKSFMSIKEGDYNPLFIPVAVMTAFSGLAFTIIMLARLKK 360
DB 314 TIGESSGIMSNPSPIQCKLDKSFMSIKEGDYNPLFIPVAVMTAFSGLAFTIIMLARLKK 373
QY 361 GKSKSRMNDP 372
DB 374 GKSKSRMNDP 385

RESULT 2
Q28629 PRELIMINARY; PRT; 376 AA.

AC Q28629;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE L-SELECTIN PRECURSOR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY, CORTEX;
RA Qian J., Marks R.M.;
RL Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL; U26535; AAA67896.1; -
DR HSSP; P14151; IKTJ.
DR InterPro; IPR000436; -
DR InterPro; IPR000561; -
DR InterPro; IPR001304; -
DR InterPro; IPR002396; -
DR Pfam; PF00008; EGF_1.
DR Pfam; PF00059; lectin_c_1.
DR Pfam; PF00084; sushi_2.
DR PRINTS; PR00343; SELECTIN.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR SMART; SM00032; CCP; 1.
KW EGF-like domain; Glycoprotein; Lectin; Signal.
FT SIGNAL 1
FT CHAIN 39 376 POTENTIAL.
SQ SEQUENCE 376 AA; 42346 MM; 59F6AD530F490947 CRC64;

Query Match 84.9%; Score 1796; DB 6; Length 376;
Best Local Similarity 84.1%; Pred. No. 1.3e-168;
Matches 311; Conservative 24; Mismatches 35; Indels 0; Gaps 0;

QY 1 MIFPMKCSOTRDLMNFKLMGWTMLCCDFLAHGTGCTYHYSEKPMNORARPCRDN 60
DB 1 MIFPMKCSOTRDLMNFKLMGWTMLCCDFLAHGTGCTYHYSEKPMNORARPCRDN 60
QY 61 YTDVAIONKAEIYELEKTLPFSSRYWIGIRKIGIMTWGNTKSLTEAENMGDEPN 120
DB 61 YTDVAIONKAEIYELEKTLPFSSRYWIGIRKIGIMTWGNTKSLTEAENMGDEPN 120
QY 121 NKKKEDCEVEIYIKRNKDAGKNDACHKLKAALCTYASCPMCSGHECEVEIINNHTC 180
DB 121 NKKKEDCEVEIYIKRNKDAGKNDACHKLKAALCTYASCPMCSGHECEVEIINNHTC 180
QY 181 NCDVGYGPOCQVIOCEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLGIEET 240
DB 181 NCDVGYGPOCQVIOCEPLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLGIEET 240
QY 241 CGPFGMWSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTACTPTGSEGTLLGKKK 300
DB 241 CGPFGMWSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTACTPTGSEGTLLGKKK 300
QY 301 TIGESSGIMSNPSPIQCKLDKSFMSIKEGDYNPLFIPVAVMTAFSGLAFTIIMLARLKK 360
DB 301 TIGESSGIMSNPSPIQCKLDKSFMSIKEGDYNPLFIPVAVMTAFSGLAFTIIMLARLKK 360
QY 361 GKSKSRMND 370
DB 361 GKSKSRMND 370

RESULT 3
Q63762 PRELIMINARY; PRT; 372 AA.

AC Q63762;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE LYMPHOCYTE MEMBRANE PROTEIN A.11.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=95369821; PubMed=7543874;
RA Sackstein R., Meng L., Xu X.M., Chin Y.H.;
RT "Evidence of post-transcriptional regulation of L-selectin gene expression in rat lymphoid cells.";
RL Immunology 85:198-204(1995).
DR EMBL; S79523; AAC60710.2; -
DR HSSP; P14151; IKTJ.
DR InterPro; IPR000436; -
DR InterPro; IPR000561; -
DR InterPro; IPR001304; -
DR InterPro; IPR002396; -
DR Pfam; PF00008; EGF_1.
DR Pfam; PF00059; lectin_c_1.
DR Pfam; PF00084; sushi_2.
DR PRINTS; PR00343; SELECTIN.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR SMART; SM00032; CCP; 1.
KW EGF-like domain; Glycoprotein.
SQ SEQUENCE 372 AA; 42471 MM; 7DFD125610DD6E4A CRC64;

Query Match

78.8%; Score 1667; DB 11; Length 372;

Best Local Similarity 77.2%; Pred. No. 6,5e-156;
Matches 287; Conservative 35; Mismatches 50; Indels 0; Gaps 0;

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QY 1 MIFPMKCOSTQRLDLMNIFKLMGWTMLCCDFLAHHGTCWTHYSEKPMNQARRFCDNYTDLVAI 60
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 MIFPMKCOSTQRLDLMNIFKLMGWTMLCCDFLAHHGTCWTHYSEKPMNQARRFCDNYTDLVAI 60
QY 61 YTDLVAIQNKAEIELEKTLPEFSRYTWIGIRKIGTWVGTNKSLEAEENMGDEPN 120
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 61 YTDLVAIQNKAEIELEKTLPEFSRYTWIGIRKIGTWVGTNKSLEAEENMGDEPN 120
QY 121 NKKNKEDCVETIYIKRNKADGKNDACCHKLAALCYTASCPWSCSHGCEVELINNHTC 180
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 121 NKKNKEDCVETIYIKRNKADGKNDACCHKLAALCYTASCPWSCSHGCEVELINNHTC 180
QY 181 NCDVGYGPOQLVIOCEPLEADELGTMDCTHPGFNFSSQCAFSCSEGTNLGIEETT 240
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 181 NCDVGYGPOQLVIOCEPLEADELGTMDCTHPGFNFSSQCAFSCSEGTNLGIEETT 240
QY 241 CGPFGMWSPEPTCOYVIOCEPLAPDLGIMNCSPHPLASFSTSACTFICSEGTLLGKKK 300
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 241 CGPFGMWSPEPTCOYVIOCEPLAPDLGIMNCSPHPLASFSTSACTFICSEGTLLGKKK 300
QY 301 TICSSGIMNSPFIQKLDKSFMSIKEGDYNPLFIPVAVMTAFSGLAFIIMLARLKK 360
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 301 TICSSGIMNSPFIQKLDKSFMSIKEGDYNPLFIPVAVMTAFSGLAFIIMLARLKK 360
QY 361 GKRSKRSMDPY 372
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 361 GKRSKRSMDPY 372

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RESULT 4
ID 095509 PRELIMINARY; PRT; 616 AA.
AC 095509;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DJ780M13.1.3 (SELECTIN P (GRANULE MEMBRANE PROTEIN 140 KDA, ANTIGEN
   CD62, GMP140)) (ISOFORM 3) (FRAGMENT).
GN SELP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Howden P.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
EMBL; AL022146; CA1814.1; -.
DR HSSP; P16109; IKJD.
DR InterPro; IPR000436; -.
DR InterPro; IPR000561; -.
DR InterPro; IPR001304; -.
DR InterPro; IPR002396; -.
DR Pfam; PF00008; EGF_1;
DR Pfam; PF00059; Lectin_C; 1.
DR Pfam; PF00084; sushi; 6.
DR PRINTS; PR00343; SELECTIN.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR SMART; SM00032; CCP; 1.
DR EGF-like domain; Glycoprotein.
KW NON_TER 616
FT SEQUENCE 616 AA; 6735 MW; 35CD4BFADE61D724 CRC64;
SO

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Query Match 43.1%; Score 911; DB 4; Length 616;
Best Local Similarity 50.6%; Pred. No. 3e-81;
Matches 158; Conservative 47; Mismatches 107; Indels 0; Gaps 0;

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QY 8 QSTQRLDLMNIFKLMGWTMLCCDFLAHHGTCWTHYSEKPMNQARRFCDNYTDLVAI 67
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 11 QRFQRYVFGISQLCFSAISLITNOKREVAAMWYHSTKAYSNMISRKYCONRTYDVAI 70
QY 68 QNKAEIELEKTLPEFSRYTWIGIRKIGTWVGTNKSLEAEENMGDEPNKKKED 127
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 71 QNKAEIELEKTLPEFSRYTWIGIRKIGTWVGTNKSLEAEENMGDEPNKKKED 130
QY 128 CVELIYIKRNKADGKNDACCHKLAALCYTASCPWSCSHGCEVELINNHTCNDVGY 187
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 131 CVELIYIKRNKADGKNDACCHKLAALCYTASCPWSCSHGCEVELINNHTCNDVGY 190
QY 188 GPQCOLVIOCEPLEADELGTMDCTHPGFNFSSQCAFSCSEGTNLGIEETTGPFGNW 247
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 191 GPCEYVRECELELDPQVILMNCSPHPLASFSTSACTFICSEGTLLGKKK 250
QY 248 SDEPTCOYVIOCEPLAPDLGIMNCSPHPLASFSTSACTFICSEGTLLGKKK 307
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 251 TNKPGCLAQCPPLKIPERGNTCLHSAKAFQHSQSCFCEGFPALVGPVYQCTASG 310
QY 308 TWSNPSPIQKL 319
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 311 VMTAPAPVCAL 322

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RESULT 5
ID 095507 PRELIMINARY; PRT; 740 AA.
AC 095507;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DJ780M13.1.1 (SELECTIN P (GRANULE MEMBRANE PROTEIN 140 KDA, ANTIGEN
   CD62, GMP140)) (ISOFORM 1) (FRAGMENT).
GN SELP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Howden P.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
EMBL; AL022146; CA1814.2; -.
DR HSSP; P16109; IKJD.
DR InterPro; IPR000436; -.
DR InterPro; IPR000561; -.
DR InterPro; IPR001304; -.
DR InterPro; IPR002396; -.
DR Pfam; PF00008; EGF_1;
DR Pfam; PF00059; Lectin_C; 1.
DR Pfam; PF00084; sushi; 8.
DR PRINTS; PR00343; SELECTIN.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR SMART; SM00032; CCP; 1.
DR EGF-like domain; Glycoprotein.
KW NON_TER 740
FT SEQUENCE 740 AA; 81095 MW; 3B5F70A45B1A3CD4 CRC64;
SO

```

Query Match 43.0%; Score 909; DB 4; Length 740;
Best Local Similarity 50.3%; Pred. No. 5.9e-81;
Matches 157; Conservative 48; Mismatches 107; Indels 0; Gaps 0;

```

QY 8 QSTQRLDLMNIFKLMGWTMLCCDFLAHHGTCWTHYSEKPMNQARRFCDNYTDLVAI 67
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 11 QRFQRYVFGISQLCFSAISLITNOKREVAAMWYHSTKAYSNMISRKYCONRTYDVAI 70
QY 68 QNKAEIELEKTLPEFSRYTWIGIRKIGTWVGTNKSLEAEENMGDEPNKKKED 127

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Db      71 QNKNKIDYLNKTVLPYSSYYWIGIRKNNKKTWGTWGTGKKALTLNEANWADNEPNKRNNED 130
      128 CVELYIKRNDAGKWNDDACHIKLKAALCYTASCOPMSCSGHGEVEIINNHTCNDVGY 187
      131 CVELYIKSPSPAGPWNWNEHECLKKHAKALCYTASCDMSCKOGELLETIGNTVSCYGFY 190
Qy      188 GPQCQVLYOCEPLAPDLGTMCTHPPGNFSSFCASFSCSECTNLGIEETTCGPGNM 247
      191 GPECEYVREGGELELPQHVLAMNCNCHPLGNFSFNQSCFHCITDGIQVNGPKLECLASGIW 250
Db      248 SSEPPTQVYIOCEPLAPDLGIMNCNCHPLASFSFTSACFTICSEGTLLGKKTTCSSG 307
      251 TNKRPQCLAAQCPPLKIPERGNMTCLHSKAKAFQHSSCSFSCGEFALVGEVYVQCTASG 310
Qy      308 IMSNPSPIQOKL 319
      311 VMTAPAVCAIKAI 322
Db

RESULT 6
ID      095508      PRELIMINARY;      PRT;      740 AA.
AC      095508;
DT      01-MAY-1999 (TREMBLrel. 10, Created)
DT      01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT      01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE      DJ780M13.1.2 (SELECTIN P (GRANULE MEMBRANE PROTEIN 140 KDA, ANTIGEN
DE      CD62, GMP140)) (ISOFORM 2) (FRAGMENT).
GN      SELP.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Howden P.;
RL      Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
DR      EMBL; AL022146; CAA18143.1; -.
DR      HSSP; P16109; IKJD.
DR      InterPro; IPR000436; -.
DR      InterPro; IPR000561; -.
DR      InterPro; IPR001304; -.
DR      InterPro; IPR002396; -.
DR      Pfam; PF00008; EGF_1.
DR      Pfam; PF00059; lectin_c; 1.
DR      Pfam; PF00084; sushi; 8.
DR      PRINTS; PR00343; SELECTIN.
DR      PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR      PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR      PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR      SMART; SM00032; CCP; 1.
DR      SMART; SM00032; CCP; 1.
DR      EGF-like domain; Glycoprotein.
KW      NON_TER
FT      CHAIN
FT      SIGNAL
SQ      SEQUENCE 740 AA; 81389 MW; 1D2E35ED93745CE CRC64;

Query Match      42.4%; Score 898; DB 4; Length 740;
Best Local Similarity 50.6%; Pred. No. 7.2e-80;
Matches 158; Conservative 45; Mismatches 109; Indels 0; Gaps 0;

Db      8 OSTORDLMNIFLWGMTCMCDLHAHGTCTYHYSEKPMNORARPCRDNYDLVAI 67
      11 ORFOVHVFGISQLLCEFSALISLTNOKVEAAWTYHSTRKAYSMSRYCCQNRRTYDLVAI 70
Qy      68 ONKATIEVLEKLPSPRSRYWYTGIRKIGIWTWGTNKSILFEARNWGDGEPNNKKNED 127
      71 QNKNKIDYLNKTVLPYSSYYWIGIRKNNKKTWGTWGTGKKALTLNEANWADNEPNKRNNED 130
Db      128 CVELYIKRNDAGKWNDDACHIKLKAALCYTASCOPMSCSGHGEVEIINNHTCNDVGY 187
      131 CVELYIKSPSPAGPWNWNEHECLKKHAKALCYTASCDMSCKOGELLETIGNTVSCYGFY 190
Qy      131 CVELYIKSPSPAGPWNWNEHECLKKHAKALCYTASCDMSCKOGELLETIGNTVSCYGFY 190

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Qy      188 GPQCQVLYOCEPLAPDLGTMCTHPPGNFSSFCASFSCSECTNLGIEETTCGPGNM 247
      191 GPECEYVREGGELELPQHVLAMNCNCHPLGNFSFNQSCFHCITDGIQVNGPKLECLASGIW 250
Db      248 SSEPPTQVYIOCEPLAPDLGIMNCNCHPLASFSFTSACFTICSEGTLLGKKTTCSSG 307
      251 TNKRPQCLAAQCPPLKIPERGNMTCLHSKAKAFQHSSCSFSCGEFALVGEVYVQCTASG 310
Qy      308 IMSNPSPIQOKL 319
      311 VMTAPAVCAIKAI 322
Db

RESULT 7
ID      028290      PRELIMINARY;      PRT;      754 AA.
AC      028290;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT      01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE      CELL ADHESION MOLECULE PRECURSOR (FRAGMENT).
GN      GMP140.
OS      Canis familiaris (Dog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedata; Canidae; Canis.
OX      NCBI_Taxid=9615;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Manning A.M., Sanders W.E. Jr., Kukiela G.L., Dore M.,
RA      Rosenbloom C.L., Hawkins H.L., Michael L.H., Entman M.L., Smith C.W.,
RA      Beaudet A.L., Anderson D.C.; to the EMBL/Genbank/DBJ databases.
RL      Submitted (MAR-1995) to the EMBL/Genbank/DBJ databases.
DR      EMBL; M88170; AAA63789.1; -.
DR      HSSP; P16109; IFSB.
DR      InterPro; IPR000436; -.
DR      InterPro; IPR000561; -.
DR      InterPro; IPR001304; -.
DR      InterPro; IPR002396; -.
DR      Pfam; PF00059; lectin_c; 1.
DR      Pfam; PF00084; sushi; 8.
DR      PRINTS; PR00343; SELECTIN.
DR      PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR      PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR      PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR      PROSITE; PS01186; EGF_2; 1.
DR      SMART; SM00032; CCP; 1.
DR      SMART; SM00032; CCP; 1.
KW      Cell adhesion; EGF-like domain; Glycoprotein; signal.
KW      NON_TER
FT      CHAIN
FT      SIGNAL
FT      SIGNAL
SQ      SEQUENCE 754 AA; 82303 MW; F0438EBA521E773 CRC64;

Query Match      41.8%; Score 884; DB 6; Length 754;
Best Local Similarity 50.5%; Pred. No. 1.7e-78;
Matches 151; Conservative 46; Mismatches 102; Indels 10; Gaps 0;

Qy      19 KLMGWTMLCCFLAHGTCTYHYSEKPMNORARPCRDNYDLVAIONKAEIYLEK 78
      7 KILCFSVLIFELIKOEKAVAGTNYSTRKAYSMSRYCCQNRHYDLVAIONKKEIAYLND 66
Db      79 TLPSRSRYWYTGIRKIGIWTWGTNKSILFEARNWGDGEPNNKKNEDCVELYIKRND 138
      67 VIFYNYSTYWYTGIRKINDKTWGTGKKPLTEAEANWADNEPNKRNNKQDCVELYIKSLA 126
Qy      139 AGKWNDDACHIKLKAALCYTASCOPMSCSGHGEVEIINNHTCNDVGYGPQCQVLYOCE 198
      127 PGKWNDEPCWKRKALCYTASCDMSCKOGELLETIGNTVSCYGFYSGPEYVREG 186
Db      128 CVELYIKRNDAGKWNDDACHIKLKAALCYTASCOPMSCSGHGEVEIINNHTCNDVGY 187
      131 CVELYIKSPSPAGPWNWNEHECLKKHAKALCYTASCDMSCKOGELLETIGNTVSCYGFY 190
Qy      139 PLEAPDLGTMCTHPPGNFSSFCASFSCSECTNLGIEETTCGPGNMSSSEPPTQVIO 258

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RESULT	12	
Q9EST7		
ID	Q9EST7	PRELIMINARY;
AC	Q9EST7;	PRT; 3567 AA.
DT	01-MAR-2001	(TREMBLrel. 16
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)
DE	POLYDOM PROTEIN PRECURSOR.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
SC	STRAIN=C3H/HENSIC.	

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RX PubMed-11062057;
RA Gilges D., Vinit M.-A., Callebaut I., Coulombel L., Cacheux V.,
RA Romeo P.-H., Vigon I.,
RT "Polydom" : a secreted protein with pentraxin, complement control
RT protein, epidermal growth factor and von Willebrand factor A
RT domains";
RL Biochem. J. 352:49-59(2000).
DR EMBL: AF206329; AAC32160.1; -.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 3567 AA: 387391 MW: 8FBA8276E12293E5 CRC64;

Query Match 11.7%; Score 248.5; DB 11; Length 3567;
Best Local Similarity 28.4%; Pred. No. 3.8e-15;
Matches 62; Conservative 33; Mismatches 94; Indels 29; Gaps 7;

OY 138 DAGKNDADCHKLKALCYATSCQPMSCSGHCEVEIINNTNCNDGVY--GPOCOLVI 195
DB 1731 DNGSMNGISFSCLDYDCAVGS----DCEHASCILNTNGSVSCNPPYTGDKNCAEPV 1786
OY 196 QCEPLEAPELGTMDCTHPFGN-ESFSSQCAFSESGEGLTGLIEETTCGPFQNMSSPEPTC 254
DB 1787 KCAKPEPENG-----HSSGRIYVGTAVTFESCEDEGHELVGVSTTLETGEMDRLRPSC 1841
OY 255 QVIOCEPLAPDGLIMNCSPHPLASFSTSACTFICSGTELICKKTKITCESSGIWNSNP 314
DB 1842 EALISGCVPPVPENGVGVS---AFTYGSKYVYKCDKGYTLSDGESACIASSGWSHSP 1897
OY 315 ICOKLDSF-SMIREGDPNLFIPVAVMTAFSGLAFI 351
DB 1898 VCELVKCSQPEDINNGKY-----ILSGITVL 1923

RESULT 13
O9YVR4 PRELIMINARY; PRT; 1124 AA.
AC O9YVR4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE FW GENE PRODUCT.
GN FW OR CG1500.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RC MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Cealiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Souton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Abmayyan A., An H.-J., Andrews-Plamkoch C., Baldwin D.,
RA Ballow R.M., Basu A., Bayendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mel M.-H., Ileguam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Liu X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskens D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gdbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
DR EMBL: AE003487; AAF48125.1; -.
DR HSSP: P02749; 10UB.
DR FLYBase: FBgn0001083; fw.
DR InterPro: IPR000436; -.
DR InterPro: IPR001304; -.
DR Pfam: PF00059; lectin_c; 1.
DR Pfam: PF00084; sushi; 11.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
DR SMART: SM00032; CCP; 1.
SQ SEQUENCE 1124 AA: 123051 MW: COEB0528A415F34A CRC64;

Query Match 11.7%; Score 247.5; DB 5; Length 1124;
Best Local Similarity 25.5%; Pred. No. 1.3e-15;
Matches 86; Conservative 40; Mismatches 122; Indels 89; Gaps 18;

OY 38 CWTYHSEKPMQORARFCRDNTDLVAIONKAEIEYLEKTLPSRS-----YYWIGIR 92
DB 231 CYDFHIT-KGSEFDKQAQICQTGDLVHDFRGATSSIISELRKSELKPOLWIAQ 289
OY 93 KIGGI---WTWGTNKSILTEAENMGDEPNKRNKEDVEIYIKRNDAK--WNDD 145
DB 290 KEPGITSRTWKVAVND---VYQKPTWGMQDPNNYNGEONCVL-----DGRNMLMNDV 340
OY 146 ACHKLKALCTTASCQPMSCSGH-----GCEVEII-----NNHTC 180
DB 341 GCN--LDYLHPTICQHSPLSCSPDAQONTTVYMKRFTLGEKIQTCPKSHLLQOTEREC 398
OY 181 NCDVGYG--GPOCOLVIOCEPLEAPELGTMDCTHPFGN-----SFSQCAFSCSEGT 231
DB 399 RLDTGWSGSSPTCKYV-DGSL--PEL-----KFGSIHSEERTSGVAITYSCHENY 448
OY 232 NLTGIEETTCGPFQNMSSPEPTCOVIO--EPLSAPDLGIMNCSPHPLASFST-----S 283
DB 449 TLINENNTNCAMDG-WSGKQPECLVDMCPDPPIAGDGV-----RFNDKRAGS 495
OY 284 ACTFICSGTEFLICKKTKITCESSGIWNSNPSPICOKLD 320
DB 496 TATVYCEPGYVLVEBALISGLGGEWSSKTPSCRFVD 532

RESULT 14
P9158 PRELIMINARY; PRT; 974 AA.
AC P9158;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE EURONED.
GN FW OR CG1500.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

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RN [1]
 RP SEQUENCE FROM N.A.
 RA Leshko-Lindsay L., Corcos V.G.:
 RL Development 0:0-0(0)
 DR EMBL: U70270; AAB36703.1; -
 DR HSSP: P02749; 1008
 DR FlyBase: FBgn0001083; fw.
 DR InterPro: IPR000436; -
 DR InterPro: IPR001304; -
 DR Pfam: PF00059; lectin.c; 1.
 DR Pfam: PF00084; sushi.10
 DR PROSITE: PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.
 DR PROSITE: PS00641; C_TYPE_LLECTIN_2; 1.
 DR SMART: SM00032; CCP; 1.
 SQ SEQUENCE 974 AA; 107557 MW; A406335FB6726757 CRC64;

Query Match 11.2%; Score 237.5; DB 5; Length 974;
 Best Local Similarity 25.2%; Pred. No. 1e-14;
 Matches 85; Conservative 39; Mismatches 124; Indels 89; Gaps 18;

QY 38 CMTYHSEKPMNQRARFCRDNYTDLVAIQNAELEYLKTLPFSR-----YWTGIR 92
 DB 49 CYFPHIT-KESPDKAQAIKQKGHLVHDFRGATSYILSELRRKSELKPOLWIGAQ 107
 QY 93 KIGGI---WTWVGTKSLTEAEENMGDEPNKKKEDCEVEIYIKRNDAGR--WMD 145
 DB 108 KEGITSRTWKVNGD---VYKPTWGKDQPNVYNGEQNCVVL-----DGNMILMDV 158
 QY 146 ACRKLAALCYTASCPWSSGSH-----GECVEIT-----NNHTC 180
 DB 159 GCN--LDYHFLICQHSPLSCGSPDAQONTVMGKFTLGKIKYQTPKGHSLGQTEREC 216
 QY 181 NCVGVYGG--POCQVIOCEPLEAPELGTMDCTHPPGNF-----SFSSQCAFSCSEGT 231
 DB 217 RLDGTSSGSPPTKRY-DCGSL--PEL-----KFGSIHMSERISFGVAVATYSCHENT 266
 QY 232 NLTGIEETTCGPPGNNSSPEPTQVIOG---EPLSAPDLGIMNCSHPLASFST-----S 283
 DB 267 TLIGNENRRCAMDG-MSGKQPECLVDMCPDPPIAGGDV-----RNDKRAGS 313
 QY 284 ACFPICTSEGTILGKKTICSESGISNPSPTQKAD 320
 DB 314 TATYFCEPGVIVGEALISGILGEGWSSKPTSCRFVD 350

RESULT 15
018849

PRELIMINARY; PRT; 868 AA.

ID 018849;
 AC 018849;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
 DE C54G4.4 PROTEIN.
 GN C54G4.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilkinson J.;
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-94150718; PubMed=7906398;
 RA Wilson R., Ahnscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,

RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL: 275533; CA99822.1; -
 DR InterPro: IPR000436; -
 DR InterPro: IPR001304; -
 DR Pfam: PF00084; sushi.4.
 DR PROSITE: PS00641; C_TYPE_LLECTIN_2; 1.
 DR SMART: SM00032; CCP; 1.
 SQ SEQUENCE 868 AA; 95322 MW; 5D57C332C70405CD CRC64;

Query Match 11.2%; Score 236; DB 5; Length 868;
 Best Local Similarity 22.3%; Pred. No. 1.3e-14;
 Matches 84; Conservative 48; Mismatches 128; Indels 116; Gaps 18;

QY 2 IFPMKCGSTORDLNIFFKLMGWTMLCCDFLAHNGTYCWTYHSEKPMNQRARFCRDNY 61
 DB 339 VSPWOCNQGOMEVYGF-----GMCYASRDEQ-TDMLGQRKCLDRG 381
 QY 62 TDLVAIQNAELEYLKTLPFS---RSYWIIGIRKIGITWVGTKSLTEAEENMGD-- 116
 DB 382 STLPLRIDSTRGLRSALSASSAKAFYWGASSMTEMRV-----DGEVGS 433
 QY 117 ---GEPMKKKEDCEI-----YIKRNDAGKNDACRKLAAALCYTASCPWSSG 166
 DB 434 DWPGPSVPVPSASEAVLLARPLEMKWVPASQTA--WNSFLCS-KPKFC-----TSP 482
 QY 167 GHGECVEI-INNT-----C-NCVGY-----YGPQCLV 194
 DB 483 GYGEAKYVFFSSISVATIGLCFYSCDSGLDGIHQRECAENGRWGTSPNCTKRSCAV 542
 QY 195 IOCEPLEADELGTMDCTHPPGNFS-----FSQCAFSCSEGTNLGTIETT----- 240
 DB 543 RQWK-----FGRIKLKLTTLFSEVEYECSSNGMILANSPPSYSLRV 587
 QY 241 CGPFGWSSPEPTCOYIOCEPLSAPDLGIMNCSHPLASFSTACTFICSEGTILGKK 300
 DB 588 CGSDGIWSSGSEPTCELYDC---GRPL-IANGRVDESSTFESAAVYCHOGFRILGPES 643
 QY 301 TICSSGISNPSPTC 316
 DB 644 LMGDRGEMQRPATPFC 659

Search completed: October 13, 2001, 03:02:16
 Job time: 424 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2001, 23:49:05 ; Search time 189.31 Seconds
(without alignments)
7492.630 Million cell updates/sec

Title: US-09-119-209-1

Perfect score: 2259

Sequence: 1 GAATTCACAGTGTCTGCTT.....CCGCCACACACTGGAATTC 2259

Scoring table:

IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 22: /cgnl_9/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2259	100.0	2259	20	AAV08321 Human lymphocyte h
2	2255.8	99.9	2259	14	AAO44243 Human DNA. Homo s
3	2255.8	99.9	2259	16	AAO92802 Human LHR cDNA. H
4	2255.8	99.9	2259	16	AAT05869 Human LHR cDNA. H
5	2255.8	99.9	2259	17	AAT30003 Human lymphocyte c
6	2255.8	99.9	2259	19	AAV19012 Homo sapiens lymph
7	2254.2	99.8	2259	14	AAO43154 Human lymphocyte h
8	2251.8	99.7	2259	13	AAO12118 Sequence encoding
9	2241.6	99.2	2260	12	AAO23623 Human lymphocyte h
10	2241.2	99.2	2262	13	AAO24987 Sequence encoding
11	2127.8	94.2	2350	17	AAT14723 Human Leu8 antigen

12	2127.8	94.2	2350	21	AA50596 Human T-cell spect
13	2126.2	94.1	2350	13	AAQ21184 Encodes T lymphocy
14	2126.2	94.1	2350	19	AAV63460 Human Leu8 antigen
15	2126.2	94.1	2350	20	AAV81217 Human Leu8 antigen
16	2087.6	92.4	2330	15	L-selectin cDNA. L
17	2086	92.3	2330	14	AAO35142 LAM-1 B125 cDNA. c1
18	2076.4	91.9	2330	14	AAQ38839 Sequence of LAM-1
19	2076.4	91.9	2330	18	AAT72270 Human lymphocyte-a
20	2074.8	91.8	2330	14	AAO37304 LAM-1 cDNA from pl
21	2058.8	91.1	2337	11	AAO05871 Sequence encoding
22	2033.4	90.0	2330	13	AAO31767 Human LAM-1. Homo
23	1273.4	56.4	1914	21	AA506332 Human T-cell speci
24	1271.8	56.3	1914	13	AAO22500 Encodes T lymphocy
25	970.2	42.9	138169	21	AAA34791 Human adenosine re
26	970.2	42.9	141589	21	AAE20913 Human ELAM-1 poly
27	970.2	42.9	141589	21	AAE21127 Human low adenosin
28	970.2	42.9	141589	21	AAE21152 Human adenosine re
29	970.2	42.9	141589	21	AAA35005 Human adenosine re
30	970.2	42.9	141589	21	AAA35030 Human adenosine re
31	970.2	42.9	146981	21	AAE21442 Human ELAM-1 poly
32	922.2	40.8	1696	15	AAO71015 Lym-1 gene exon X
33	856.8	37.9	2214	13	AAQ23624 Murine lymphocyte
34	856.8	37.9	2214	13	AAQ24988 Sequence encoding
35	856.8	37.9	2214	14	AAO43155 Murine lymphocyte
36	856.8	37.9	2214	14	AAO44244 MLHR DNA. Mus mus
37	856.8	37.9	2214	16	AAO92803 Mouse LHR cDNA. M
38	856.8	37.9	2214	16	AAT05870 Mouse LHR cDNA. M
39	856.8	37.9	2214	17	AAV08322 Mouse lymphocyte c
40	856.8	37.9	2214	20	AAV08322 Mouse lymphocyte h
41	848.8	36.7	2214	12	AAO12119 Sequence encoding
42	828.8	36.7	1496	11	AAO05542 Sequence encoding
43	817.8	36.2	2219	19	AAV19013 Mus musculus lymph
44	885.2	17.1	531	15	AAO71009 Lym-1 gene exon I
45	385.2	17.1	5666	14	AAQ38840 Sequence of exons

ALIGNMENTS

RESULT	ID	AAV08321 standard; DNA; 2259 BP.	Human T-cell spect
AAV08321	AAV08321		
AC	AAV08321		
XX			
DT	02-FEB-1999	(first entry)	
XX			
DE	Human lymphocyte homing receptor coding sequence.		
XX			
KW	Lymphocyte homing receptor; LHR; lymphocyte cell-surface glycoprotein;		
KW	lymphocyte binding; endothelium; graft rejection; inflammation; therapy;		
KW	arthritis; autoimmune disease; lymphoma metastasis;		
KW	lymphocyte accumulation; human; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	US5840844-A.		
XX			
PD	24-NOV-1998.		
XX			
PF	10-AUG-1995;	95US-0513278.	
XX			
PR	23-FEB-1989;	89US-0315015.	
PR	31-OCT-1991;	91US-0786149.	
PR	06-MAY-1993;	93US-0059029.	
PR	10-AUG-1995;	95US-0513278.	
XX			
PA	(GERTH) GENENTECH INC.		
PA	(REGC) UNIV CALIFORNIA.		
PI	Lasky LA, Rosen SD, Singer MS, Stachel SE;		
DR	WPI; 1999-034122/03.		

Db 1741 ttcttaactccagatgaagtaatgggggtcctctgcaagtctgaagaagcttccatttcgacgtg 1800
 QY 1801 TAGCCTCGCCGCTGTGATTTGGACCATCTCTATTAACTGGCTTCAGGGCTCCGCCACTT 1860
 Db 1801 tagccctcgccgtctgtgaatggaacatccatttaacgtgctcagggctcccccacctt 1860
 QY 1861 CTTGAGCCACCTCTCTTTTTCAGTTGGTGTGACTTCACACGCTGACATGTCATGATGACCA 1920
 Db 1861 ctctagccacccctctcttctcaagtgtgcgtcaactccacacctagacatcgaagtgcga 1920
 QY 1921 AGCAAAAGAGAGAGAGAGAAATAGCCTCGCGGCTTTTTCAGTTGGGGGCTTTGCTGTG 1980
 Db 1921 agcaaaagagagagagagaaatagcctcgcggtttttagtttggtgggttttgctgt 1980
 QY 1981 TTCTCTTTATGAGACCATCTCTATTCTTTATAGTCAATGTTTCTTTTATCAGATATTA 2040
 Db 1981 ttctctttagagacccatctccattctctatagtcaatgattcttcttatacgaatatla 2040
 QY 2041 TTAGTAAAGAAACATCATCGAATGCTAGCTGCAAGTCACTCTTTGATGATCATATGG 2100
 Db 2041 tttagtaagaataacatcacgaatgctagctgcaagtgcacatctcttgatgcatatg 2100
 QY 2101 AAGAGTTAAAGAGGTGAGAAATTCCTTGATTCACAAATGAATGCTCTCTTTCCCTG 2160
 Db 2101 aagagttaaagaggtgagaaatctcttgatcacaaatgcatgtcttcccttccctg 2160
 QY 2161 CCCCCGAACCTTTTATCATCTTACCTAGATTCATATTCCTTTAAATTCATCTCAGGC 2220
 Db 2161 ccccccgaaccttatacctactacctaagattcacatattctttaaattcatctcaggc 2220
 QY 2221 CTCCCTCAACCCGACGCGGCCGCGACACATCGAATTC 2259
 Db 2221 ctccctcaaccccgagcgccgacacatcgaatlc 2259

RESULT 2

AA044243
 ID AA044243 standard: DNA; 2259 BP.

XX AA044243;

DT 11-JAN-1994 (first entry)

XX HULHR DNA.

XX Human; murine; lymphocyte; cell surface glycoprotein; homing receptor;

KM LHR; endothelium; lymphoid tissue; signal; domain; complement binding;

KM carbohydrate binding; epidermal growth factor-like; egf; intracellular;

KM transmembrane binding; cytoplasmic; ligand binding partner protein;

XX TMD; LBPP; ss.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

PI Capon DJ, Lasky LA;
 XX MPI; 1993-226664/28.
 DR P-PSDB; AAR38908.
 XX
 PT New lymphocyte homing receptor immunoglobulin fusion
 PT polypeptides) - used to inhibit binding of lymphocytes in
 PT therapeutic and diagnostic uses
 XX
 XX Disclosure; Fig 1; 44pp; English.

The sequences given in AA044243-44 encode human and murine lymphocyte cell surface glycoprotein (LHR) respectively. The proteins encoded by these sequences mediate the binding of lymphocytes to the endothelium of lymphoid tissue. LHR is a glycoprotein which contains a signal domain, a carbohydrate binding domain, an epidermal growth factor-like (egf) domain, at least one complement binding domain repeat, a transmembrane binding domain (TMD) and a charged intracellular or cytoplasmic domain. The murine and human amino acid sequences show a high degree of overall homology (83%), however degrees of homology between the various domains is variable. These proteins may be fused to a ligand binding partner protein (LBPP) which causes an increase in the half life of the LHR. The fusions may be used therapeutically to compete with the normal binding of lymphocytes to lymphoid tissue. They may be used in organ or graft rejection and for the treatment of inflammation.

Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other;

Query Match 99.9%; Score 2255.8; DB 14; Length 2259;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2257; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 61 gagacccttgtgctaaatgcaagaggtcaatggctgacagagactagagagaccaa 120
 QY 121 GCAAAGCCATGATTTCCATGGAATGTCAGAGCCACCAAGAGGACTATGGAACATCT 180
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 QY 181 TCAAGTTGTGGGGGTGAGCAATGCTGTGATTTCTGTGACATCATGAACTTACT 240
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Db 661 acacccctgcaactgtgagtggtggtactatggtgccccagtgctcagcttgatcagtg 720
QY 721 AGCCTTTGAGGGCCCCGAGCTGGGTACATGAGCTGACTACCCCTTTGGAACCTTCA 780
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Db 721 agcctttgagggccccagagctggtgaaacagctgactacccctttggaactca 780
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RESULT 3
AA092802
ID AA092802 standard; cDNA: 2259 BP.
XX AC
XX AA092802;
DT 01-DEC-1995 (first entry)
XX DE
XX Human LHR cDNA.
KW Lymphocyte homing receptor; lymphocyte cell surface glycoprotein;
KW LHR; ligand binding partner; immunoglobulin; constant region;
KW antibody engineering; immunomodulator; ss.
XX OS
XX Homo sapiens.
XX FH
XX Key 129..1247 Location/Qualifiers
XX CDS 186..224
XX FT sig_peptide
XX FT /*tag= a
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XX PD
XX 27-JUN-1995.
XX PR
XX 23-FEB-1989; 89US-0315015.
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.

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QY	781	GCTTCAGCTCACAATTGTGCTTCAAGCTGCTCTCAAGGAACAACTTAACTGGGATTGAG	840
DB	781	gcttcagctcacaatgtgcttcaagctcgtctctcaaggaaacaaacttaactggtattgag	840
QY	841	AAACACCTGTGGAGCCATTTTGGAAATCGGTCATCTCCAGAACCAACCTTCAGAGATTTC	900
DB	841	aaacacactgtggagcccatttggaaactggctcatctccagaaaccaactgtccagatcttc	900
QY	901	AGTGTAGCCCTCTATGAGACACAGATTTGGGGATCATGAATGTAGCCATCCCTGGCCA	960
DB	901	agtgtagccctctatcagcaaccagatttgggattcatgaaactgtagccaatccctctggca	960
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DB	961	gcttcagctttaacctctgcatgtacatcttcctcctcgaagaagaaactgtatatttggga	1020
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DB	1021	agaagaaaaacatttgyaatcatctgyaatccgytccaatccctagttccaatagtccaa	1080
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DB	1201	taaaaaaaggcaaacaaatccaagagaagtaagaaagccaatataaaccgccccttgg	1260
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DB	1261	aaagaaaaatcttcttggaaatactataaatacatagagatccctttaatcccttcagaaagct	1320
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DB	1321	tttgtgtgtggccacctctctacgctcaacaalgaagtggtcttccctcagtgcatctggag	1380
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DB	1381	atttctacccgacaagagttccttcagcttccatcttgcctccctcaattatctcccaacc	1440
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DB	1441	ccgagccacagggcttataacagcttcagcttcttcttccctcagggagaaacaataa	1500
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DB	1561	tcttgttttccagtttcaattcagtgctgtactgtgacagacactcttaaatgaagtc	1620
QY	1621	AAATTTGATACATATGTGAATATGAGACTGATTTTCTGCAGTCAAAATTCACGTGCTC	1680
DB	1621	aaatttgatacatatgtgaatatgagactgatttctgcagatccaatlttaagtcgtc	1680
QY	1681	TTTCTGATACTGTGAGAGTCACTCTTATGAAGTTCAAAAAGTCTACGCTCTCTTTC	1740
DB	1681	tttctgatactgtgagagttcactcttataagaaagttcaaaaagcttaagctctctcttc	1740
QY	1741	TTTTCTAACTCCAGTAGAATATGAGGGGTCTGCTCAAGTTGAAAGAGTCCATTTTGCACTG	1800
DB	1741	ttttctaaactccagtagaataatggggctcgtccctcaagttcgaaaggtccattcttgcactg	1800

QY	1801	TAGCGTCGCGCTGTGTAATTTGACCACTTCTTAATTAAGTCGCTTACAGGCGCTCCCACTT	1860
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QY	1861	CTTAGCGCACTCTCTTTTCAGTTGGGCGTACATCCACACGTAGCAATGCATGAGATGCA	1920
Db	1861	cttaagcaactctcttcttcaagtctggaactccacacccagatcccaagatgcga	1920
QY	1921	AGCAAAAGAGAGAGAGAGACAAAATAGCGTCGCGGCTTTTATAGTTTGGGGCTTTTGCTGT	1980
Db	1921	agcaaaagagagagagagagaatagctgcgcggtctttagtcttggtggtctgcgt	1980
QY	1981	TTTCCTTTTATGACAGCCATTCCTCTTAATTTCTTAATAGTCAATGTTTCTTTTATCAGCATATA	2040
Db	1981	tctctttaaagagcccatctccatctctataagtaagttcttcttataccagatla	2040
QY	2041	TTTAGAAGAAACATCACTGAATAATGAGTCGAATGCATCTCTTTGATGTGCATATGG	2100
Db	2041	ttagtaagaaaactcactctgaatagtctagctgaagtgcacatctcttgatgataatg	2100
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Db	2161	ccccagaacttataccacttaccatagatccaacatacttctaattcaatccatcaggc	2220
QY	2221	CTCCCTCAACCCACGGGGCGGCAGACACACTGGAATTC	2259
Db	2221	ctccctcaaccccaagggcgccagacacactggaattc	2259

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DT	31-OCT-1996	(first entry)
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DE	Human lymphocyte cell surface glycoprotein (HLHR) coding sequence.	
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KW	Immunoglobulin; transmembrane receptor; adhesion; targeting;	
KW	diagnosis; therapy; drug delivery; antiviral; neuromodulator;	
KW	immunomodulator; cell adhesion; graft rejection; inflammation;	
XX	metastasis; ss.	
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OS	Homo sapiens.	
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FT	CDS	129..1247
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PN	US5514582-A.	
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PD	07-MAY-1996.	
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PE	23-FEB-1989;	89US-0315015.
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PR	22-NOV-1989;	89US-0440625.
PR	23-FEB-1989;	89US-0315015.
PR	16-DEC-1991;	91US-0808122.
PR	08-DEC-1992;	92US-0986631.
PR	21-JAN-1994;	94US-0185670.
XX		
PA	(GETH) GENENTECH INC.	
XX		

PI Capon DJ, Lasky LA;
 XX
 DR WPI; 1996-238773/24.
 DR P-PSDB; AAR98106.

PI Nucleic acid encoding hybrid immunoglobulin comprising the ligand
 binding site of a receptor fused to Ig constant region - useful for
 PT diagnosis and treatment e.g. of inflammation
 XX

PS Example 2; Figure 1; 41pp; English.

XX
 CC A hybrid immunoglobulin chain comprising the ligand binding site of
 CC a single transmembrane receptor without an active transmembrane
 CC region; fused at its C-terminus with the N-terminus of an
 CC immunoglobulin constant region. The receptor is not a member of the
 CC immunoglobulin super family, nor a multiple subunit polypeptide
 CC encoded by discrete genes. The hybrid immunoglobulin chain combines
 CC the adhesion/targeting of a ligand binding partner (LBP) with the
 CC effector functions of immunoglobulin and can bind to and/or activate
 CC more than one ligand. It can be used diagnostically for the in
 CC vitro assay of LBP and their targets; or therapeutically to deliver
 CC LBP such as toxins, enzymes, growth factors to particular cells.
 CC Typical applications are as antiviral, neuromodulating and
 CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
 CC treating graft rejection; inflammation; metastasis of lymphoma etc.)
 CC The immunoglobulin component increases plasma half life and
 CC facilitates purification while deletion of the transmembrane region
 CC facilitates recovery, improves aqueous solubility and removes
 CC potentially immunogenic epitopes.

SQ Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other;

Query Match 99.9%; Score 2255.8; DB 17; Length 2259;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 2257; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 DB 61 gaaaccccttgtgctgctgctgctgctgctgctgctgctgctgctgctgctgct 120
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QY 2101 AAGAGTTAAACAGGTGGAGAAATTCCTTGATTACACATGAATGCTCTCTTCCCTG 2160
Db 2101 aagagttaaacaggtgagaaatctcttgatcacaaatgaaatgctctctctccctg 2160
QY 2161 CCCCCAGAACTTTATCCACTTACCTAGATCTACATATTCTTAAATTTCACTCAGGC 2220
Db 2161 cccccagaaactttatccacttaccatgagatctacacatcttcttaaatcttcaatcc 2220
QY 2221 CTCCTCTCAACCCCGAGGGCGCCGACACACTGGAATTC 2259
Db 2221 ctccctcaaccccgagggcgccgacagactggaattc 2259

```

RESULT 6

AAV19012
ID AAV19012 standard; DNA; 2259 BP.

AC AAV19012;

DT 17-AUG-1998 (first entry)

DE Homo sapiens Lymphocyte homing receptor (LHR) gene.

KM Lymphocyte homing receptor; LHR; HuLHR; organ; graft; rejection;
KW treatment; inflammatory disorders; rheumatoid arthritis;
KW autoimmune diseases; lymphoma metastasis; control; lymphocyte;
KW accumulation; ds.

OS Homo sapiens.

FX Key Location/Qualifiers

FT CDS 129..1247

FT /tag= a

FT /product= lymphocyte homing receptor

XX US5714147-A.

XX 03-FEB-1998.

XX 23-FEB-1989; 89US-0315015.

XX 22-NOV-1989; 89US-0440625.

```

PR 23-FEB-1989; 89US-0315015.
PR 19-DEC-1991; 91US-0808122.
PR 08-DEC-1992; 92US-0986931.
PR 21-JAN-1994; 94US-0185670.
PR 26-MAY-1995; 95US-0451848.
XX
PA (GETH ) GENENTECH INC.
PI Capon DJ, Lasky LA;
XX
PI WPI; 1998-129805/12.
XX
DR P-PSDB; AAW37781.
XX
PT Prevention of lymphocyte attachment to endothelial cells - using
PT chimeric molecule comprising lymphocyte homing receptor and
PT immunoglobulin constant region
XX
PS Disclosure; Fig 1; 43pp; English.
XX
CC The sequence is that encoding a human lymphocyte homing receptor
CC (LHR) which may be used in the construction of a chimeric molecule
CC comprising an LHR fused at its C terminus to the N terminus of an
CC immunoglobulin constant region. This can be used for the prevention
CC of lymphocyte attachment to endothelial cells. Such a method may
CC be used for preventing organ or graft rejection, for treating
CC inflammatory disorders, e.g. rheumatoid arthritis or other
CC autoimmune diseases, for controlling lymphoma metastasis and
CC for treating conditions in which there is an accumulation of
CC lymphocytes.
XX
SQ Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other;

Query Match 99.9%; Score 2255.8; DB 19; Length 2259;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2257; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAATTCAGTGTGCTGCTCTTCACCTGCAGCAGCAGCAGCTCTTGGCAAGACCT 60
Db 1 gaattccagtgctgctcttcctcactgcagccagcaactctcttggcaagacct 60
QY 61 GAGACCTTGTCGAATGCAAGGGCTCAATGGCTCAGAGAACTAGAGAGACCAA 120
Db 61 gagaccttgctgaagtcagagagcctcaatggctcagagaaactagagaaagaccaa 120
QY 121 GCAAAAGCATGATATTTCCATGGAATGTGAGACACACAGAGGACTTGAACATCT 180
Db 121 gcaaaagcatgatatctccatggaatgtaagagcaccagagagattatgaaactct 180
QY 181 TCAAGTTGTGGGGTGAGCAATGCTGTGTAATTTCTGGCAGATCATGAACCTACT 240
Db 181 tcaagttgtggggtgagcaatgctgtgtgtaatttctggcagatcatgaacctact 240
QY 241 GCTGGAATTCATTTATTCGAAAAAACCCATGAACCTGGCAAGGCTTAGAAGATTCTGCC 300
Db 241 gctgggaattcatatttcgaaaaaacccatgaacctggcaaggcttagaagattctgcc 300
QY 301 GAGACATTACACAGATTTTATGTCATACAAAACAAGGCGGAATTTGATATCTGGAGA 360
Db 301 gagaacaattacacagatttattgtgccatacaaaaagaaggggaattgatatctggaga 360
QY 361 AGACTCTGCCCTTCAGTCTTACTAGTGAATGGAATCCGAGATAGAGAAATAT 420
Db 361 agactctgcccttcagctcttactacaggaataacccgaaagataaggagaaatc 420
QY 421 GAGCGTGGTGGGAAACCAAAATCTCTCACTGAAGAAGAGAACTGGGGAGATGCTG 480
Db 421 gagcgtgggtgggaaaccaaactctctcactgaagaagagaaactggggagatgctg 480
QY 481 AGCCCAACAACAAGAGAGAGAGAGAGCTGCTGAGATCTATCAAGAAACAAG 540
Db 481 agcccaacaacaagaagagagagagagctgctgagatctatcatcaagaagaacaag 540

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QY 541 ATGAGGCAATGAGACGATGACCGCTGCACAACTAAAGCAGCCCTGTATTACAG 600
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 Db 541 atgaggaatgagacgaigagcgctgcacaactaaagcgccctgtattacag 600
 |||||
 QY 601 CTCTTGCCAGCCCTGGTGCATGACGTGGCCATGGAAGATGTGTAAATCATTAATC 660
 |||||
 Db 601 ctcttgccagccctggtcatgagtgccatggaatgtgtagaatcatcataatc 660
 |||||
 QY 661 ACACCTGCAATGTGATGGGGTACTATGGGGCCGAGTGCACCTGTGATTTAGATG 720
 |||||
 Db 661 acacctgaactgtatggtggttaactatgggcccagtgacagctgtgattcaagt 720
 |||||
 QY 721 AGCCTTGGAGGCCCGAGAGTGGGTACCATGAGACTGACTACCCCTTGGAACTTCA 780
 |||||
 Db 721 agccttggagggcccagagctgggtaccatgagctgactacccttggaaactca 780
 |||||
 QY 781 GCTTACACTCAGANTGTGCTTACGCTGCTGTGAAGAACAACTTACTGGGATTGAG 840
 |||||
 Db 781 gcttcaactcagatgtgcttcaagctgtgaagaaacttaactggtgattgaag 840
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 Db 841 aaacacactgtgacaccttggaaactgtgcatctccaagaaacctgtcaagtgatc 900
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 QY 1081 AATTGCAAAATTTCTCAATGATTAAGAGGGTATTTAAACCCCTCTTATTCAG 1140
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 Db 1081 aatttgcaaaaatlttctcaatgattaaaggggtgatttaaaccctcttattccag 1140
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 QY 1141 TGGCAGTCATGTTAGTGCATCTCTGCTGGTGGCATTTATCATTTGGCTGGCAAGGAT 1200
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 Db 1141 tggcagtcagtgttactgcatcttctggtgtgcatltaatttggcggcaaggatc 1200
 |||||
 QY 1201 TAAAAAAGGCAAGAAATCCAGAGAGATGATGACCATTAAATCGCCCTTGGTG 1260
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 Db 1201 taaaaaaggaagaatccaagaagatgatagccataatlaatcgccttgggtg 1260
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 QY 1261 AAAGAAATTTCTGGAATCTATAAATCATGAGATTCCTTTAAATCCTTCATGAACGTT 1320
 |||||
 Db 1261 aaagaaatcttctggaatacttaaaaaatcatgataatccttcaatccatgaaacgt 1320
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 QY 1321 TTGTGTGTGGGCACTCTACGTCAAACATGAAGTGTGTTCCCTTACGTGATGGGAG 1380
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 Db 1321 ttgtgtgtgggcaactctacgtcaaacatgaagtgtgttcccttaccgtgacatctggag 1380
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 QY 1381 AATTTCACCGACCAACAGTCTCCATGAGCTTCATTTGCCCCCTCATTTATCCCTAAC 1440
 |||||
 Db 1381 atttcaaccgaccaaagcttccatgacttccattgccccctcatltaaccctaac 1440
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 Db 1441 cccagcccaagtggttatacagctcagcttcttcttcttcttcttcttcttcttcttct 1500
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 |||||
 Db 1501 gaccataagggaagatcatgtggaataataaagatgtgacttcttcttcttcttcttct 1560
 |||||
 QY 1561 TCTTGTTCATTTCAATTCAGTGTGATGATGACAGACACTTCTAAATGAAGTGC 1620
 |||||
 Db 1561 tcttgttctcagttcaatcagctgctgactgataagacacttctaaatgaagtg 1620
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 QY 1621 AAATTTGATACATATGTGTAATGTGACATCAGTTTCTTGACAGATCAAAATTTACGTCGTC 1680
 |||||

Db 1621 aaattgatcatatgtgataatgagacagtttcttctgcaataatltcaagtcgctc 1680
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 Db 1681 ttctgatactgtggaggtacactcttataagaagtccaataaagctcaagctctctctc 1740
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 QY 1741 TTTCTAACTCCATGAAATGATGGGTCCTGCTCAAGTTGAAAGAGTCTTATTTGACTG 1800
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 Db 1741 ttcttaactcagatgaatgaatggtgtccgtcgaagtgtgaagagcttccatttgcactg 1800
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 QY 1801 TAGCTTGCCGCTGTGGAATTTGAGACATCTTATTTACTGCTTCAGGCTGCCACCTT 1860
 |||||
 Db 1801 tagcctgcgcgtctgtgaattgacatactcttaactgactgcttcaagctcccaactt 1860
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 QY 1861 CTTCAGCACCTCTCTTTTTCAGTTGCTGACTTCCACACTAGACATCATGAGTGCCA 1920
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 Db 1861 cttcagcacactctcttcttcaagttgctgacttccacactagcatctcatgagtgcca 1920
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 QY 1921 AGCAAAAGGAGAGAGAAATAGCCGCGCGGTTTATGTTGGGGCTTTGCTGT 1980
 |||||
 Db 1921 agcaaaaggagagagagaaatagcctgcgcggttlttagtltgggtgttgcgt 1980
 |||||
 QY 1981 TTCCCTTTATGAGACCCATTCCTATTCTTATAGTCAATGTTCTTTATCAGATATTA 2040
 |||||
 Db 1981 ttccctttagagaccatctcctattcttataagtaagatgttcttcttatacagatata 2040
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 QY 2041 TTATGTAAGAAACATCAGCAAAATGCTAGCTCAAGTCAATCTCTTTGATGTCAATAG 2100
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 Db 2041 ttatgtaagaatacatcactgaaatgtagcttgcaagtgaacatctctttagatgtcata 2100
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 QY 2101 AAGAGTTAAACAGGAGGAGAAATTCCTGATTTCATGAAATGCTGCTTCCCTG 2160
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 Db 2101 aagagttaaacaggttggagaatctcctgattcaaatgaatgctcctcttccctg 2160
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 QY 2161 CCCCCAGAACTTTATTCACCTTACCTAGATTCTACATATTTCTTAAATTTGATCAGGC 2220
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 Db 2161 cccccaagacttltacacttaactagattctacatatctttaaattcatcctcagc 2220
 |||||
 QY 2221 CTCCCTCAACCCGACGCGGCGCCGACACATGGAATTC 2259
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 Db 2221 ctccctcaaccccgagggcgccgacacatgtgaattc 2259
 |||||

RESULT 7
 ID AA043154 standard: CDNA: 2259 BP.
 XX AA043154;
 AC 08-OCT-1993 (first entry)
 XX
 DE Human Lymphocyte Homing Receptor coding sequence.
 KW HuLHR; lymphocyte binding inhibition; lymphoma metastasis;
 KM transplant rejection; ss.
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS -129..1247
 FT FT /*tag= a
 FT sig_peptide /product= HuLHR
 FT 186..224
 FT /*tag= b
 XX
 XX US216131-A.
 XX 01-JUN-1993.
 XX PD
 XX 23-FEB-1989; 89US-0315015.
 XX PF
 XX 23-FEB-1989; 89US-0315015.
 PR

PR 31-OCT-1991; 91US-0786149.
XX (GETH) GENENTECH INC.
XX Lasky LA, Rosen SD, Singer MS, Stachel SE, Yednock TA;
PI WPI; 1993-188588/23.
DR P-PSDB; AAR37960.
XX
XX Human and murine lymphocyte homing receptors to treat graft
PT rejection and inflammation - comprise carbohydrate binding,
PT epidermal growth factor and complement binding domains
XX
XX Example 2; Fig 1; 32pp; English.
XX A human peripheral blood lymphocyte cDNA library in lambda gcl10 was
CC screened with a 2.2kb EcoRI insert of the murine Mel14 antigen clone
CC (i.e. a murine LHR sequence). The largest EcoRI insert (2.2kb) was
CC isolated and sequenced. The ORF codes for 372 amino acids with a mol.
CC wt. of approximately 42,200. Comparison of the HuhR cDNA with the
CC previously determined murine LHR sequence (AA043155) showed 83%
CC homology.
XX
XX Sequence 2259 BP; 635 A; 515 C; 490 G; 619 T; 0 other;
SQ

Query Match 99.8%; Score 2254.2; DB 14; Length 2259;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAATTCAGTGGTGGCTGCTCTCCACCTGACAGACAGACACTCCCTTGGCAAGAGCCT 60
DB 1 gaattccagtgctgctgctccaccctgcagacagacacccctcttggaaggacct 60
QY 61 GAGACCTCTGTGCTAAGTCAGAGGCTCAATGCGCTGCAGAAAGACTAGAGAGCA 120
DB 61 gagacctctgtctaaagtcgaagtgctcaatgctgcagaaagactagaagagccaa 120
QY 121 GCAGAGCCATGATATTTCATGGAATGTACAGACCCAGAGGACTTATGGACATCT 180
DB 121 gcaaaagccatgatatttcattggaatgtacagacccagagacttatagaaacatc 180
QY 181 TCAAGTGTGGGGGTGAGCAATGCTGTGTGATTTCCGGGCAATCATGGAACCTACT 240
DB 181 tcaagtgtgggggtgagcaatgctgtgtgatttcgggcaatcatggaacctact 240
QY 241 GCTGACATTACATTTATCTGAAAAACCCATGAACCTGCAAAAGGCTAGAAATCTGCC 300
DB 241 gctgacattacatttattctgaaaaacccatgaacctgcaaaaggctagaagatctgcc 300
QY 301 GAGACATTTACACAGATTATGTTGCCATACAAAACAGGCGAATTGAGTATCTGAGA 360
DB 301 gagacatttacacagattatgttgccatacaaaacagggcggaattgagatctgaga 360
QY 361 AGACTGTGCTTCATCTGCTTTACTACTAGTAGTAATCCGGAATAGAGGATATAT 420
DB 361 agactgtgcttcattctgctttactactagtagtaatccggaatagagggatatat 420
QY 421 GGACGTGGTGGGAACCAAAATCTCTCACTGAAGACAGAGAACTGGGAGATGTTG 480
DB 421 ggacgtgggtgggaaccaaactctctcactgaagaagcaggaactctgggagatggtg 480
QY 481 AGCCCAACAACAAGAAACAAGAGAGACTGCGTGAATCTATATCAAGAGAAACAAG 540
DB 481 agcccaacaacaagaacaagagagactgctggaatctatactaaagagaacaag 540
QY 541 ATGCAGAGCAAAATGGAAGCATGACGCTGCGACAAATAAGGACGCGCTGTACACAG 600
DB 541 atgcagagcaaaatggaaagcatgacgctgcgcacaaataaagagcgccctgttacaag 600
QY 601 CTTCTTGCCAGCCCTGTGTCATGCAGTGGCCATGGAGAAATGTGTGAATCATCAATATC 660
DB 601 ctctcttgccagccctgtgctcatgcagtggccatggagaaatgtgtgaatcatcaat 660

QY 661 ACACTGCAACTGTGATGTGGGGTACTATAGGCCCCAGATGTCAGCTTGTGATTCAGTGTG 720
DB 661 acactgcaactgtgatgtggggactatagggcccccagatgtcagcttgtgattcagtgctg 720
QY 721 AGCCTTTGAGGAGCCCGAGAGCTGGGTACATGAGACTGTACTCACCCTTGGAAACTTCA 780
DB 721 agcctttgagagcccgagagctgggtacatgagactgtactcacccttggaaacttca 780
QY 781 GCTTCAGCTCAGAGTGTGCTTCAGCTGCTGTGAAGAACAACTTAAGTGGATTGAAG 840
DB 781 gcttcagctcagagtgcttccagctgctgtgaagaaacttaactacggaattgaag 840
QY 841 AAACCACTGTGGACCAATTTGGAACGTGCATCTCCAGAACCAACTGTCAAGTGAATTC 900
DB 841 aaacacctgtggaccaatttggaaactgtcatctccagaaaccaactgtcaagtgatc 900
QY 901 AGTGTAGCCTCTATCAGCAGCAGATTTGGGATCATGAACTGTAGCCATCCCTGGCCA 960
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QY 961 GCTTCACCTTTACCTCTGCATGTGTAACCTTCATCTGCTCAGAGAACTGACTTAATTGGGA 1020
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QY 1021 AGAAGAAAACCATTTGTGATTCATCTGGAATCTGTGTAATCCTACTAGCCAAATGTCAA 1080
DB 1021 agaagaaaacctttgtgatctcatctggaatctgtgtaaatcctactagccaaatgtcaa 1080
QY 1081 AATTGACAAATGTTCTCATATATTAAAGAGGTGATTTAAACCCCTTTATCTTAC 1140
DB 1081 aattgacaaatgttctcatattttaaagagtgattttaacccctttatcttaccag 1140
QY 1141 TGGCAGTCATGTTACTGCACTTCTGGGTTGGCATTTATCATTTGGCTGGCAAGAGAT 1200
DB 1141 tggcagtcattgttactgcacttctgggttgccatttatcatcttgctggcaagagat 1200
QY 1201 TAAAAAAGCAAGAAATCCAAAGAAAGTATGAATGACCCATTTAAATGCCCTTGCTG 1260
DB 1201 taaaaaagcaagaaatccaaagaaagtatgaatgacccatttaaatgaccttggtg 1260
QY 1261 AAAGAAATCTCTGGAATTAATAATCATGAGATCCTTTAAATCCCTCATGAAAGCTT 1320
DB 1261 aaagaaatctctggaaattataatcatgagatccttttaaatccctcatgaaagctt 1320
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DB 1381 atttctacccgaccaaacttccttcagcttcatttcgcccctcatltaaccctcaac 1440
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DB 1441 cccagccacagagtgttatatacagctcagcttttgccttcttcgggagaaacaaataa 1500
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DB 1501 gaccatataagggaagaatctcatgtgaatttaagatgctgacttgtcttggac 1560
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DB 1561 tcttgtgttctcagtttcatttcagtgctgtgatacgaagaaactcttaaaagaaagtcgc 1620
QY 1621 AAATTTGATACATATGTGAATATGACTAGTTTCTTGACAGATCAAAATTTCAAGTCTGC 1680
DB 1621 aaatttgatatacatatgtgaatatgactagtttcttgacagatcaaaatttcaagctgc 1680
QY 1681 TTCTGTATACCTGTGAGAGTACACTCTTATAGAAAGTTCAAAAAGTCTACGCTCTTTC 1740
DB 1681 ttctgtatacctgtgagaggtacacctcttatagaaagttcaaaaagttcagctctctcttc 1740

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QY 1801 TAGGCTGGCGGTCTGTGAATTGGACCATCTATTAACTGGCTTCAAGGCTCCGACCTT 1860
    |||||||
Db 1801 tagctgcgcgtctgtgaattgacccatttaactgtctcagcgtcccccacctt 1860
QY 1861 CTTCAGCACCTCTCTTTTTCAGTGGTGAATCTTCACACTGACATCTCATGTAGTGCCA 1920
    |||||||
Db 1861 cttagcgcacctctcttcttcagtgctgaactccacccagcactcatgagtgcca 1920
QY 1921 AGCAAAAGAGAGAGAGAGAGAAATAGCCTCGCGGTTTTTGTAGTTGGGGTGGTGTGT 1980
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Db 1981 ttccctttagagaccattccattcttctatagtcagtcttcttcttaccagata 2040
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QY 2161 CCCCAGAACTTTATTCACATCTAGATTTACATATTTCTTAATTCATCTCAGGC 2220
    |||||||
Db 2161 cccccagaaacttaccacttaccatgactcactgactcactcattctttaaattcactcagc 2220
QY 2221 CTCCTCAACCCGAGGGGGCGGCAGACACACTGGAATTC 2259
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Db 2221 ctccctcaaccccgagggcgccgacgacactggaattc 2259

RESULT 8
AAQ12118
ID AAQ12118 standard; DNA; 2259 BP.
XX
AC AAQ12118;
XX
DT 09-SEP-1991 (first entry)
XX
DE Sequence encoding human lymphocyte cell surface glycoprotein (LHR).
XX
KW Ligand binding partner; lbp; stable plasma protein; spp; antiviral;
KW immunomodulatory; neuromodulatory; receptor mediated abnormality; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 129..1247
FT /*tag= a
FT sig_peptide 186..224
FT /*tag= b
FT mat_peptide 243..1244
FT /*tag= c
XX
PN WO9108298-A.
XX
PD 13-JUN-1991.
XX
XX 21-NOV-1990; 90WO-US06849.
XX
XX 22-NOV-1989; 89US-0444625.
XX
XX (GETH ) GENENTECH INC.
XX
XX Capon DJ, Lasky LA;
XX
XX WPI; 1991-193202/26.
XX
DR

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DR P-PDB; AAR12469.
XX
PT New hybrid immunoglobulin(s) - for use as diagnostic reagents for
PT ligand binding molecules and to treat organ and graft rejection
PT and inflammation.
XX
PS Disclosure; Fig 1; 67pp; English.
XX
CC The gene product may be used as a ligand binding partner in combina-
CC tion with a stable plasma protein eg. IgG1-IgG4, IgA, IgE, IgD or IgM.
CC The fusion product is joined by N- or C-terminal groups, preferably
CC the N-terminal of the FC region of the spp is linked to the C-terminal
CC of lbp. They may be used to provide antiviral, immunomodulatory
CC and neuromodulatory treatment as well as in treatment of receptor
CC mediated abnormalities.
XX
SQ Sequence 2259 BP; 634 A; 516 C; 487 G; 618 T; 4 other;

Query Match          99.7%; Score 2251.8; DB 12; Length 2259;
Best Local Similarity 99.7%; Pred No. 0;
Matches 2253; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GAAATCCAGTGTGCTGGCTTCTCCTCACCTGACACAGACACTCCCTTGGCAAGACT 60
    |||||||
Db 1 gaattccagtgctgtgcttccctcactgcmnmacgacactcccttggcaagact 60
QY 61 GAGACCCCTGTGCTAAGTCAAGAGGCTCAATGGCTGCGAAGAACTAGAGAAGCA 120
    |||||||
Db 61 gagaccctgtgcttaagtaagagagctcaatggctgcgaaagaaactagaagaagca 120
QY 121 GCAAAGCCATGATATTTTCATGGAATGTCAAGACACCAGAGGGAGCTATGAGACT 180
    |||||||
Db 121 gcaaaagccatgatatcttccatggaatgtcagagacaccagaggaactatggaact 180
QY 181 TCAAGTTGTGGGGGTGGACAAATGCTGTGTGATTTCCGTGGACATCATGGAACACT 240
    |||||||
Db 181 tcaagttgtgggggtggacaaatgctgtgtgatttccgtggacatcatggaacct 240
QY 241 GCTGGACTTACCATATTTCTGAAAAAACCCATGATGCGCAAAAGGCTTGAAAGATTCT 300
    |||||||
Db 241 gctggaacttaccattatctgaaaaaacccatgaactgycaaaggttagaagattctcc 300
QY 301 GAGACAATTAACAGATTAGTGGCCATACAAACAGCGGAATTGATCTGAGAGA 360
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Db 301 gagacaattaacagatttagtggccatatacaaaagcggaattgattctgagaga 360
QY 361 AGACTCTGGCCCTTCAAGTGTCTTACTACTGATGGAATCCGAAATAGAGAGAAATAT 420
    |||||||
Db 361 agactctggcccttcaagtgtcttactactgatatgagatccggaagatagagaaat 420
QY 421 GGACGTGGGTGGGAACCAAAATCTCTCACTGAAGAGAGAGAACTGGGAGATGGTG 480
    |||||||
Db 421 ggacgtgggtgggaaccaaactctctcactgaagagagaaactggggaatgggtg 480
QY 481 AGCCCAACAACAAGAAAGAAAGAGAGAGAGAGAGAGAGATATATCAAGAAACAAG 540
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Db 481 agcccaacaacaagaagaagaagagagagagagagagagatatacaagaagaagaag 540
QY 541 ATGACGCAAAATGAGACGATGAGCGCTGCCACAAACTTAAAGGAGACCCCTGTGTACA 600
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Db 541 atgacgcaaaatgagacgatgagcgctgcccaaaacttaagggagacccctgttaca 600
QY 601 CTCTTGGCAGCCCTGGTCATGAGTGGCCATGAGGAATGTGTGAATATCATCAATATC 660
    |||||||
Db 601 ctcttggcagccctggtcatgagtggtggcccatgaggaatgtgtgaatatactcaat 660
QY 661 ACACCTGCAACTGTGATGTGGGTACTATGTGGGCCAGAGTGCACCTGTGTAGTGTG 720
    |||||||
Db 661 acacctgcaactgtgatgtgggtactatgtgggccagagtgacactgtgtatcagtg 720
QY 721 AGCCTTGGAGGCCCCAGAGCTGGGTACCATGACTGTACTACCCCTTGGAAACTTCA 780
    |||||||

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Db	721	agccttvgagagcccaagagctvggtgtaaccaatgactgtatccacccttvggaaacttca	780
Qy	781	gcttcagctcACAGTgtgTccCTTcAGCTgcGTcTGAAGaGAAcCAAcTTAAcTGGaATTGAAG	840
Db	781	gcttcagctcAACagtgctgcttcaagctgcctctcgaaggaacaaacttaactgattgag	840
Qy	841	AAACcACCTGTGGACcATTtTGAAAcTGTcATCTcCAGAcCAAcCTGTcAAGTATTC	900
Db	841	aaacacactgtgagccacttctggaactgtgtcaatccacgaacaaacgtcaagtgatlc	900
Qy	901	AGTGMAGCCCTATTCAGACcCAAGATtTGGGGATcATGAAcGTGAAGCCATCCCGTGCA	960
Db	901	agtgvgagccctctacagccacagatcttvgggtatcaatgaaactgtagccatccccgtgcca	960
Qy	961	GCTTCAGCTTAACTcCTGCATGTACCTTcATGTGCACAAAGAAcTGAATTAAATTGGGA	1020
Db	961	gcttcagcttaccctcctgcagttaactctcatcctgcacgaagaactgagttaattggga	1020
Qy	1021	AGAAAGAAAcCCATTGTGAATCATCTGGAATCTGTCAATCTGATCCATATGTCAAA	1080
Db	1021	agaagaaaacccatttgyaatcatctcgaatctgtgtcaaaatccctagtccaatagtcaaa	1080
Qy	1081	AATTGGACAAAAcGTTTCTCAATATTAAGAGAGGTATTAACCCCTCTTCAATCCAG	1140
Db	1081	aattggaacaaaagtttctcaatgattaagaaggtgpatataaaccctctcatlccag	1140
Qy	1141	TGGcAGcATcGTATTCAGcAATTCCTcTGcGGGTGGcATTATTCATtTGcGGcCAAGcAGAT	1200
Db	1141	tggcagcatcagtttaactgcgactcttcgggttggcatltaactcttgcgcgcaaggaat	1200
Qy	1201	TAAAAAAAGcCAGAAATTCcAAGAGAAcGTATGATAGCCcATTTAAATCGCCCTTGcGTG	1260
Db	1201	taaaaaaagcagaagaatcccaagaagatgaatgaaacccatataaatgcgccccttggtg	1260
Qy	1261	AAAGAAATTTCTTGGAATACTAAAAATCATGAGATCCTTTAAATCCTTCATGAAAcGTT	1320
Db	1261	aaagaaatcttctggaataactaaataatcatgagatcctttaaactcttccatlgaaacgtt	1320
Qy	1321	TTTGcGTGGTGcACCTCTCTcAGTCAAAcCATAGAAcGTGTCTCTTcAGTcCAATcTGcGGAAG	1380
Db	1321	tttggtggtgagacctctccatcgttcaaacatgaagtggttctcctcaagtgcatactcgggaag	1380
Qy	1381	ATTTCTACCCGACCAACAGTTCTCTCAGCTTCcATTTCGCCCCATTTATCCCTCAAC	1440
Db	1381	attctacccggaaccaacagttcctctcagctcatcatttgcgccctcatltaaccctcaac	1440
Qy	1441	CCCAcGCCCAcAGGTtTATATACGCTcACGTTTtGTCTTTCTcAGAGAAcCAAAATTA	1500
Db	1441	cccaagcccaacagtggttataacagctcaagcttltgtcttctctcgtgaggaacaaataaa	1500
Qy	1501	GACATTAAGGGAAAGATTCATGTGGAATATAAGATGGCTcACCTTCTCTCTTGAC	1560
Db	1501	gacataaaggaagaagatctcaatgvgaaataaagaatgvgacttgcctctcttcgac	1560
Qy	1561	TCTGTtTTTcAGTTTCAATTCACGTGTATCTGTATGAGAcAGAcACTTCTTAAATGAAGTGC	1620
Db	1561	tctgttcttcaagttcaatcattcagtgctgtactgtatgaagaagcactcttaataaagtgac	1620
Qy	1621	AAATTTGATACATATGTGAATATGAcCTcAGTtTCTTGcAGATCAAAATTCACGTCTC	1680
Db	1621	aaattgatataatagtgaataatgagactagtttctctgcagatcaaatlccaacgtctgc	1680
Qy	1681	TTTGcTATACGTGGAGcGTcACACTCTTATAGAAAGTCAAAAGCTcAGCTCTCTTTC	1740
Db	1681	ttcgtataaacgtgaggtacactcttaagaagaatccaanaagctcagctctcttc	1740
Qy	1741	TTTTTAACTCCAGTGAAGTATGAGGTCCCTGTCTCAAGTTGAAGAAGTcCTATTTGCACTG	1800
Db	1741	ttcttaactccagtggaagtaatgvggtctcgtcccaagttgaaaggtctcatatttgacgtg	1800
Qy	1801	TAGcCTcCGcGTCTGTGAATTGACAcATCCcTATTAATcGTGcCTTcAGGcCTCCcCAcCTT	1860
Db	1801	tagctctcgctctcgtgttaatttgacaatcctatlaaacgtgcttaaggtcccccacactt	1860

QY	1861	CTTCAGCCACTCTCTTTTCAGTGGCTACTTCCACACCTAGCATCTCAATGATGCCA	1920
Db	1861	cttcagccacctctcttcttcagttgctgacttccaccctcagcatgtcagtgcca	1920
QY	1921	AGCAAAAGAGAGAAGAGAAATAGCGTCGCGGTTTTTTAGTTGGGGGTTTTGTGTGT	1980
Db	1921	agcaaaagagagagagaaatagccgcgcgcttcttcagttcttg999cttcgcgt	1980
QY	1981	TTTCCTTTTATAGACCCATTCCTATTTCTTATAGTCMAATGTTTCTTTATACAGATATTA	2040
Db	1981	tttcctttaagagcccatcttcattcttatagtacatgtcttcttatacagatatta	2040
QY	2041	TTTAGTAGAAAAACATCTCAATGCTAGCTGCAATGACATCTCTTGATGTCTATATGG	2100
Db	2041	tttagtaagaaaaacatctcattaaatgctgctgaatgcaatctcttgatgtcataatg	2100
QY	2101	AAGAGTTAAACAGGTGAGAAATTCCTTGATTCACAAATGAATGCTGCTTCCTCCCTG	2160
Db	2101	aagagttaaacaggtgagaaatcttcgtatcacaaagaaatgctctctcttccctg	2160
QY	2161	CCCCAGAACCTTTATTCACACTTACCTAGATTCATATTCCTTTAAATTCATCTCAGGC	2220
Db	2161	ccccagaaactttatctcacttacttactagattctaatcttcttaattcaatctcagc	2220
QY	2221	CTCCCTCAACCCCAAGGGGCGCCGACACACTGTGAATTC	2259
Db	2221	ctccctcaaccccaagggcgccgacagacacttgaattc	2259
RESULT 9			
ID	AAQ23623	standard; DNA; 2260 BP.	
XX	AAQ23623;		
AC	01-SEP-1992	(first entry)	
XX			
DE	Human lymphocyte homing receptor gene.		
XX			
KW	HuLHR; LHR; binding; endothelium; immunogens; graft; organ; ss;		
KW	rejection; inflammation; rheumatoid arthritis; lymphoma metastasis.		
OS	Homo sapiens.		
XX			
FT	Key	Location/Qualifiers	
FT	CDS	129..1248	
XX		/*tag= a	
XX	US5098833-A.		
PD	24-MAR-1992.		
XX			
PF	23-FEB-1989;	89US-0315015.	
XX			
PR	23-FEB-1989;	89US-0315015.	
XX			
PA	(REGC) UNIV OF CALIFORNIA.		
XX			
PI	Laaky LA, Rosen SD, Stachel SE, Slinger MS, Yednock TA;		
DR	WPI: 1992-123385/15.		
XX	P-PSDB; AAR22802.		
PT	New DNA encoding at least one domain of lymphocyte homing		
PT	receptor - useful for treating graft rejection, inflammation,		
XX	etc.		
PS	Claim 3; Fig 1; 32pp; English.		
CC	The DNA sequence was obtd. by screening an oli50 dr primed lambda		
CC	gt10 cDNA library derived from human peripheral blood lymphocyte		
CC	mRNA obtd. from primary cells, with a 2.2 kb EcoRI insert of the		

SQ Sequence 2260 BP; 636 A; 518 C; 487 G; 619 T; 0 other;

0

QY	721	AGCCTTTGGAGGCCCCGACGCTGGTATGCATGAGACGTGTACTACCCCTTTGGAAACTTCA	780
Db	721	agccttggagggcccagagctgggtacatgactgctactcaacccttggaaattca	780
QY	781	GCTTCACCTACAGTGTGCTTCAGCTGGTCTGGAAGAACAACTTAATCTGGGATTTGAG	840
Db	781	gcttcagctcaagctgctcctcagctgctctcgtcctgaaggaaacaacttaactctggattgaag	840
QY	841	AAACCACTGTGGACATTTTGGAACTGCTCATCTCCAGAACCAACCTGTCAAGTGTATTC	900
Db	841	aaaccacctgtgagccatttggaaactgttcactccagaaacaacctgtcaagtgtatc	900
QY	901	AGTGTGAGCCTCATATGAGACCCAGATTTTGGGATCATGAACTGATGACCATTCCTGGGCCA	960
Db	901	agtgtagcctctatacgaaccaagatttgggtatcaatgaacactgtagccaacccttgcca	960
QY	961	GCTTCAGCTTTACCTCTGCAATGTACCTTCATGTGCTCGAAGAGAACTGAGTTAATTGGGA	1020
Db	961	gcttcagcttacctcctcgtatgacttcctcatctgctcagaagaaactgtgatttggga	1020
QY	1021	AGAAAGAAACATTTTGGATCATCGGAATTCGGTAAATCCATGACCAATATGTTCAA	1080
Db	1021	acaaagaaaccttctgtgatacattccgtgaatccagtaaccagtaacatcagttcaaa	1080
QY	1081	AATTTGACAAAAGTTTCTCAATGATTAAAGAGAGGGTGATTAATACCCCCCTTGATTTCCAG	1140
Db	1081	aatttgacaaaagtttctcaatgattaaagaggggtgatattaaaccccttcaatccag	1140
QY	1141	TGCGCATGATGGTTACTCGATTCCTCGGTTGGCATTTATCATTTGGCTGTGGCAAGAGAT	1200
Db	1141	tggcagatcaggttactcgatctcctggttctgtgattatcatttggctgtggcaaggagt	1200
QY	1201	TAAAAAAGGCAAGAAATCCAGAGAAATATGAATGACCCATTAATGCGCCTTGAG	1260
Db	1201	taaaaaaggaagaatccaaagagaagtatgaatggccatatlaatcgtcccttgggt	1260
QY	1261	AAAAGAAATTTCTTGAATATCTAATAAATATATAGATCCTTTAAATCCTTCATGAAGAGTT	1320
Db	1261	aaagaaatattcttggatatactaaataatcagatccctttaaactccatcagtaaacgctt	1320
QY	1321	TTGTGTGTGGCAGCTCCTACGCTAAACATTAATGTGTTCCTTCAGTGATGTGGAG	1380
Db	1321	ttgtgtgtggcagctcctacgctaaacatataatgtgttccttcagtgatgtggag	1380
QY	1381	ATTTTACCCGACACACAGTTCCTTCAGCTTCATTTCCGCCCTCATTTATCCCTCAACC	1440
Db	1381	attttacccgacacaacagttcccttcagctcagcttccatcttcgcacctaatcttacc	1440
QY	1441	CCGACCCACAGGTTTATATACACTCAGCTTTTGTCTTTCTGAGGAAACAAATA	1500
Db	1441	ccgagcccaaggttatacagctcaagcttcttgccttcttcggaggaacaaataa	1500
QY	1501	GACCATTAAGGAGAAAGATTCATGTGGAATATAAAGATGGCTGACTTGTCTTTGTGAC	1560
Db	1501	gaccataagggaagagatcatatgtgataataaagatgctgacttgccttcttgac	1560
QY	1561	TCTTTCTTTTCAGTTTCAATTACAGGCTGTACTGTAGACAGACACTGTAAATGAAAGGC	1620
Db	1561	tctgttttcagttcataatccagctgctgatacttgaagaaagcaactcctaaatgaagtc	1620
QY	1621	AAATTTGATACATATGTGAATATGAGCTAGTTTCTTCSAGATCAAAATTCACCTCCTC	1680
Db	1621	aaatttgatacatatgtgataatgagctcagtttcttctgcagatcaaatcttaagctgctc	1680
QY	1681	TTTCTGTATACGTGTGAGGATCACCTTTATAGAAGTTCAAAAGCTTACGCTTCTCTTC	1740
Db	1681	tttctgtatactgtggaggtacaccttcatagaaagttcaaaagctacgctctccttc	1740
QY	1741	TTTCTAACTCCAGTGAATGATGGGCTCTGCTCAAGTTGAAGAGTCTTATTTGCACCTG	1800
Db	1741	tttctaactccagtgaaagtaatgggtctctgctcaagttgaaaggtcctacttgcacgt	1800

QY 1801 TAGCCTGCGGCTGTGTAATTTGACATCCATTTAACTGGCTTCAGAGCCCTCCACACTT 1860
|||||
Db 1801 tagctcgccgctgtgtbaattggacatccatttaacttggtcttcagagcccccaccctc 1860
QY 1861 CTTCAGCCACTCTCTTTTTCAGTTGGCTGACTTCACACCTAGCATCTCATGAGTGCA 1920
|||||
Db 1861 cttaggcacctctctcttttcagttgctgacttcacacctagcatctcatgtagtgca 1920
QY 1921 AGCAAAAGAGAGAGAGAGAGAAATAGCCTGCGCGGTTTTTATGTTGGGGTTTTGCTGT 1980
|||||
Db 1921 agcaaaagagagagagagagaaatagacctgcggtttttagtttg9999tttctgtc 1980
QY 1981 TTGCTTTATGAGAGCCATTCCTATTCTTATAGTCAATGTTTCTTTATCAGCAATTTA 2040
|||||
Db 1981 ttctctttagagagaccatctcctatcttcttataagtcattgtttcttatacagatala 2040
QY 2041 TTAGTAAGAAAACATCACTGTAATGCTAGCTGCAAGTGACATCTTTGATGATATGG 2100
|||||
Db 2041 ttagtaagaaaacatcatctgtaaatgctagctgcaagtgaactctctttagatcatatg 2100
QY 2101 AAGAGTTAAACAGGTGGAGAAATCTCTGATTCACATGAATGCTCTCTTCCCTG 2160
|||||
Db 2101 aagagttaaacaggttgagaaatctcttgatcacaaatgaaatgctctcttccctg 2160
QY 2161 CCCCAGACCTTTTATTCACCTTACCTAGATTCTACATATTCTTAAATTCATCTCAGGC 2220
|||||
Db 2161 cccccagaaactttatctcaacttaccatagatctcacaatcttcaatctcaatcaga 2220
QY 2221 CTCCTTCACCCCAACGGGGCCGCGCAGCA 2248
|||||
Db 2221 ctccctcaaccccaacggggcgcgcaagca 2248

RESULT 10

AAQ24987
ID AAQ24987 standard; DNA: 2262 BP.
XX AC AAQ24987;
XX AC
DT 22-NOV-1992 (first entry)
XX DE Sequence encoding human lymphocyte cell surface glycoprotein
DE (HULHR).
XX KM Lymphocyte cell surface glycoprotein; ligand binding protein; ss.
XX OS Homo sapiens.
XX FH Key
FT CDS 129..185 Location/Qualifiers
FT /tag- a
FT sig_peptide 186..242
FT /tag- b
FT mat_peptide 143..1247
FT /tag- c
XX US5116964-A.
XX PN 26-MAY-1992.
XX PD
XX PF 22-NOV-1989; 89US-0440625.
XX PR 23-FEB-1989; 89US-0315015.
XX PR 22-NOV-1989; 89US-0440625.
XX PA (GETH) GENENTECH INC.
XX PI Capon DJ, Lasky LA;
XX WPI: 1992-199589/24.
XX P-PSDB: AAR24026.
XX Nucleic acid encoding polypeptide fusions - comprising ligand

PT binding partner protein and immunoglobulin chain, for use in
PT diagnosis and therapy
XX
PS Disclosure; Fig 1-1 - 1-3; 43pp; English.
XX LHR mediates the binding of lymphocytes to the endothelium of
CC lymphoid tissue. Full length cDNA clones and DNA encoding the human
CC and the murine LHR (HULHR and MLHR, respectively) have been
CC identified and isolated (see AAQ24987 and AAQ24988). LHR is a
CC glycoprotein which contains the following protein domains: a signal
CC sequence, a carbohydrate binding domain, and epidermal growth
CC factor-like (egf) domain, at least one and preferably two complement
CC binding domain repeat, a transmembrane binding domain (TMD), and a
CC charged intracellular or cytoplasmic domain. LHR is used as the
CC ligand-binding partner in fusion polypeptides with an immunoglobulin,
CC for use in diagnosis and therapy.
XX
SQ Sequence 2262 BP; 635 A; 518 C; 488 G; 621 T; 0 other;

Query Match 99.28; Score 2241.2; DB 13; Length 2262;
Best Local Similarly 99.7%; Pred. No. 0;
Matches 2256; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 1 GAATTCAGTGTGCTGGCTTCTCACCCTGACAGCAGACACCTCCCTTTGGCAAGGACCT 60
|||||
Db 1 gaattcaagtgctgtcgtcttcctccacccgacagacacctccttggcaagagacct 60
QY 61 GAGACCTTGTGCTTACGTCAAGAGGCTCAATGGGCTGAGAAAGACTAGAGAGACCAG 120
|||||
Db 61 gagaccttgtgcttaagtcgaagagagctcaatgggctgagaaagactagagaagaccag 120
QY 121 GCAAAGCCATGATATTTTCATGAAATGTCAAGACACCAGAGGACTTATGAAATCT 180
|||||
Db 121 gcaaaagccatgatalttccatgtaaatgtagagacaccagagagactatgaaacatct 180
QY 181 TCAAGTTGTGGGGGTGACAAATGCTGTTGTAATTCCTGGCAATCATGAACTACT 240
|||||
Db 181 tcaagttgtgggggtgacaaatgctgttgtatctccggcacatcagaaacctact 240
QY 241 GCTGGACTTACCATTTATCTGAAAACCCATGAATGGCAAGGGCTAGAAATTCGCC 300
|||||
Db 241 gctggaacttacatatttcttgaaaacccatgaatggcgaaggcttagaaatctgcc 300
QY 301 GAGACAAATTACAGATTTAGTCCATFACAAAACAAAGCGGAATTTAGATTTGGAGA 360
|||||
Db 301 gacacaattacacagattttagtgcatalacaaaacaaagcggaattgagatctgaga 360
QY 361 AGACTGCGCCTTCAGTGTCTTACTACTGATAGGAATCCGGAAGATAGAGGAATAT 420
|||||
Db 361 agactcgccttcagtgcttcttactactgataagaaatccggaagatagaggaatct 420
QY 421 GGACGTGGGTGGGAACCAACAAATCTCTCACTGAAAGAGCAGAACATGGGAGATGGTG 480
|||||
Db 421 ggaagtgggtgggaaccaaacaatctctcaactgaaagagcaggaactgggagatggtg 480
QY 481 AGCCCAACACAGAGAAAGAGAGAGACTGCTGAGATCTATATACAGAAACAAAG 540
|||||
Db 481 agcccaaacacagagaaagagagagactgctgagatctatatacagaagaaacaaag 540
QY 541 ATGAGGCAATGGAAGATGACGCCCTGCCCAAACTAAAGGAGCCCTCTGTACACAG 600
|||||
Db 541 atgagggcaatggaaatgacgccctgcccaaaactaaaggagccctctgttaccag 600
QY 601 CTTCTGCAAGCCCTGTGTCATGATGAGGCGCATGAGAGATGTTGAATCATCAATATC 660
|||||
Db 601 ctcttcgcaagccctgtgtcatgagtgagtgccatgagagatgtgtgaatacatcaataatc 660
QY 661 ACACCTGCAACTGTGATGTGGGGTACTATAGGCCCCAGAGTGTGACCTGTGATTGAGTGTG 720
|||||
Db 661 acacctgcaactgtgactgtgggtactatagggccccagagtgacagctgtgttcagtgctg 720
QY 721 AGCCTTTGGAGGCCCGACAGAGCTGGGTACATGACATGACTACTACCCCTTTGGAAACTTCA 780

ID	Accession	Standard	CDNA	BP
Db	1801	ctgtagcctcgccgctctgtgaatttggaccatcctattacatctgcttcaggccctccac	1866	
Qy	1858	CTTCTTCAGCAGCAGCTCTCTTTTTCAGTTGGCTGACTCCAGACACTGACATCATGAGNG	1917	
Db	1861	ctcttcacagcaacctctctcttttcaagtgtgctgaattccacactagatcctcaagatg	1920	
Qy	1918	CCAGCAAAAGAGAGAAAGAGAGAAATAGCCCTGGCGGTTTTTTTAACTTGGGGGTTTTGC	1977	
Db	1921	ccaagcaaaaggagagagagagaaatagacctgacgtgcggtttttagtttggtgggtttgc	1980	
Qy	1978	TGTTTCCCTTTTATGAGACCAATTCCTATTCTTATATGTCAATGTTCTTTTATACAGTA	2037	
Db	1981	tgttcccttttatvgagccaccttccatttcttataagtaagttcttcttatacagata	2040	
Qy	2038	TATATAGTAAAGAAACATCACTGAAATGCTAGCTGCAAGTGAATCTCTTGTATGTCATA	2097	
Db	2041	tattatgaagaagaacatcatcgtgaatgctagctgcaagtgacatctctttgagtata	2100	
Qy	2098	TGGAGAGCTTAAACAGGTGAGAAATCTCTTATTCACAAATGCTCTCTTTGCC	2157	
Db	2101	tggaaagagtaaaacagtgtagaatacttctgtatcaaatgaaatgctctcttcc	2160	
Qy	2158	CTGCCCCAGAACTTTTATTCACATCTACCTAGATTACATATTTCTTTAAATTCATGCA	2217	
Db	2161	ctgccccagaaactttatcacacttactactagatcttcaacatcttcttaattcatctca	2220	
Qy	2218	GGCTTCCTCAACCCGACGGGGCGCCAGCACACTGTGAATTC	2259	
Db	2221	ggctctccctcaaccctcagggcgccgacagactggaatc	2262	

ID	Accession	Standard	CDNA	BP
XX	AA14723			
XX	AA14723	standard	CDNA; 2350 BP.	
DT	31-OCT-1996	(first entry)		
XX	Human Leu8 antigen cDNA (major transcript).			
XX	Cell surface antigen; cloning; immunoselection; immunotherapy;			
XX	therapy; diagnosis; vector; COS; Leu8; T-lymphocyte; ss.			
XX	Homo sapiens.			
XX	OS			
XX	Key	Location/Qualifiers		
XX	CDS	50..1207		
XX	FT	/tag-a		
XX	FT	1079..1514		
XX	FT	/tag-b		
XX	FT	/note="bases 1079-1514 are deleted in the shorter cDNA clone"		
XX	PM	US506126-A.		
XX	PD	09-APR-1996.		
XX	PF	25-FEB-1988;	88US-0160416.	
XX	PR	01-DEC-1992;	92US-0983647.	
XX	PR	25-FEB-1988;	88US-0160416.	
XX	PR	13-JUL-1989;	89US-0379076.	
XX	PR	13-JUL-1990;	90US-0553759.	
XX	PR	18-OCT-1993;	93US-0139273.	
XX	PA	(GEHO) GEN HOSPITAL CORP.		
XX	PI	Aruffo A, Seed B;		
XX	WP1	1996-200279/20.		
XX	P-PSDB	AAR91442.		

Db	1804	cttca-aggctccccaaccttcttcagccacacctctcttcttcagltgctgacttccacaac	1862
Qy	1902	TAGCATCTCATGAGTGGCCAGACAAAAGAGAGAAGAAATAGCCTCGCGGTCTTTT	1961
Db	1863	tagcatctcatgagtgcccaagaagaagagagaagaatagcctgcgtgtgttttt	1922
Qy	1962	AGTTGGGGGGTTTTTGGCTTTCCCTTTTATGAGACCCATTCCATTTCTTATAGTCATGT	2021
Db	1923	agttggggggttttgcctgcgttctcttcttatgagcccatctcttatagtcaatgt	1982
Qy	2022	TTCCTTTATCAGATATTATTAGTAAAGAAACATCAGTAATAGTACGTGCAAGTACA	2081
Db	1983	ttctctttatcacgatatattatagtaagaanaacctcgaatagctgcgaagtga	2042
Qy	2082	TCTCTTGATGTCATATGAAAGAGTTTAAAAACAGAGTGAAGAAATTCCTTGATTCAACATGA	2141
Db	2043	tctctttgatgctatgataggaagataaaaaagggtggagaaatccttgattcaaatga	2102
Qy	2142	AATGCTCTCCTTTTCCCTGGCCCCAGAACTTTTATGC-ACTTACCTAGATTCTACATATT	2200
Db	2103	aatgctctcctttccctgcgcccaagacctttatcgcattactagattctaataatt	2162
Qy	2201	CTTTAAATTCATCTCAGGCTCCGCCCAACCCAC	2235
Db	2163	cttcaaatctcatctcagcgtcctccctcaacccac	2197

RESULT	12
AAA50596	
ID	AAA50596 standard; cDNA; 2350 BP.

DT 19-DEC-2000 (first entry)

Human T-cell specific Leu8 antigen cDNA

KM leu8: cell surface antigen; human; immunoselection; panning;
KM immunodiagnosis; diagnosis; immunotherapy; gene therapy;
KM immune disorder; infection; asthma; immune-complex disease;
KM amyloidosis; multiple sclerosis; inflammation; antiinflammatory
ss.

OS Homo sapiens.

FH	Key	Location/Qualifiers
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ET / *tag=

PN US6111093-A

PD 29-AUG-2000

PF 28-OCT-1998; 98US-0181612

PR 01-DEC-1992

PR 13-JUL-1989

PR 13-JUL-1990

PA (GEHO) GEN HOSPITAL CORP.

PI Stamenkovic

WPI; 2000-58

XX

PT useful for i

PT diseases -

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PS Example 14; Column 69-72; 75pp; English.

CC The present sequence is that of a cDNA clone encoding a T-cell
CC specific Leu8 antigen (see AAY96138). It is 1 of 2 clones (see
CC also AAY50622) isolated from a human T-cell library by the method of
CC the invention. The method, designed to isolate cell surface
CC antigen (CSA) nucleic acids, is based upon transient expression of
CC a CSA in eukaryotic cells and physical selection of cells expressing
CC the antigen by adhesion to (penning on) an antibody-coated substrate
CC such as a culture dish. CSA nucleic acids isolated by the method of
CC the invention, and the proteins they encode, are useful for
CC immunodiagnostic and immunotherapeutic applications, including the
CC diagnosis and treatment of immune-mediated infections, diseases, and
CC disorders in animals, including humans. These disorders include
CC asthma, immune-complex disease, amyloidosis, parasitic diseases or
CC multiple sclerosis. The ability to interfere with the binding of
CC Leu8-T-cells to antigen presenting cells, or the ability to cause
CC such binding to occur on surfaces other than lymphocyte cells, can
CC be useful in diagnostics and therapy. The level of activated Leu8-
CC T-cells relative to resting Leu8+ cells could serve as a measure of
CC immune response to a particular antigen. Modification of the
CC specificity of the extracellular domain of Leu8, which mediates
CC adhesion to specific endothelial cells of lymph nodes, could serve
CC to regulate the homing potential of resting T cells. Soluble forms
CC of Leu8 could act as antiinflammatory agents by reducing lymphocyte
CC migration.

Sequence 2350 BP; 679 A; 520 C; 490 G; 661 T; 0 other;

Query Match	94.2%	Score 2127.8;	DB 21;	Length 2350;
Best Local Similarity	99.3%;	Pred. No. 0;		
Matches 2179; Conservative	0;	Mismatches 12;	Indels 4;	Gaps 4;

QY	44	CCCTTTGGCAAGACCTGTGAGACCCCTTGTGCTAGTCAAGAGGCTCATAGTGGCTGTGAGAAAG	10
Db	4	cccttgggcaagaggaacctgtgagaccttgcgttaagtaagaagagctcaatctggtctgcaagag	63
QY	104	AACCTAGAGAGGACCCACCAAGCAAGCAATGATATTTCATGTGAATAATGCACAGACCCCAAG	16
Db	64	aactagagagaggaaccaagcaaaagccagatatttccatggaataatgctcgtgagaccccaagag	122
QY	164	GGACTTATTGGAAACATCTTCAAATTGTGGGGGTGGACAAATCTCTGTTGTGATTTCTTGCC	22
Db	124	ggactatatgaaacatcttcaagtctgtgagggtgagacaatgctctgtgtgatttccgtgc	18
QY	224	ACATCATGGAGACCTACAGCTGCTGGACATTACCAATTATTCTGAAAAAACCCATGAACTGGCAAG	28
Db	184	acatacatggaacccgacctgtcgtgacttaaccattatcttgaaaaacccatggaactggaag	24
QY	284	GGCTAGGAAGATTCTGCCGAGACAAATTACACAGATTATGTTGGCATACAAACCAAGGGCGGA	34
Db	244	ggctagaagaattcttcgcgcgagacaattacacagaatttagltgcatacaaaaacaaggcgga	30
QY	344	AATTGAGTATCTGGAGAGAAGACTCTGCCCTTCACTCGTTCTTACTACTGATAGGAATTCG	40
Db	304	aattgagtatcttgcgagaagaagctctgccttccagtcgttcttactactgattagaatccg	36
QY	404	GAAAGTATAGGAGGAATTATGACAGCTGGGTGGGAAACCAACAAATCTCTCACTGAAGAAGAGA	46
Db	364	gaagataaggaagaaatagtcgctgggtgggaaacacaacaaatcttccacttgaagaagacga	42
QY	464	GAACTGGGGCAATGTGTAGCGCCAAACAAAGAAAGAAAGGAGAGCTGCGTGGAGATCTA	52
Db	424	gaacttgggggaaatggtgtgagcccaacaacaagaagaacaaggagagctctgctggaagactta	48
QY	524	TATCAGAAGAAACAAAGATGCAGGCAAAATGGAACATGATACCTTGCCACAAACTAAAGGC	58
Db	484	tatcaagaagaaacaagaatgtgcagtgcaaatgysgaacga tgaagcctctgcaccaactaaaggc	54
QY	584	AGCCCTCTGTTTACACAGCTTCTTGGCCAGCCCTGGTTCATGACAGTGGCATGGAGATGTGT	64
Db	544	agccctctgtttaaacaagctcttgcacagccctgtgtcattgaggtatgacatagaataatct	60

QY	644	AGAAATCATTAATTAATACACACTGCAACTGTATGTGGGCTACTATGGGCCCACTGTCA	703
Db	604	agaaatcataataataataccctcgcaactgtatgtggyggtactatggyccccaattgcca	663
QY	704	GCTTGTGATTAGGTGTAAGCCTTTGGGGCCCCAGAGCGGGGTACCATGGAATGTATGCA	763
Db	664	gtctgtgactcaatgtgaagcctcttgagggcccagaagctgggtacaatggaactgactca	723
QY	764	CCCCCTTGGAAACTTCAGCTTCAGCTCACAGTGTGGCTTCACCTGCTCGAAGGAACAA	823
Db	724	ctcttgggaaactcgcctcgaactcgaagctgtgcttccagctgctctcgaagaaacaa	783
QY	824	CTTAACTGCGATTGAGAAACCAACTGTGGACCACTTTGGAAACGTGCATCTCCAGAAC	883
Db	784	cttaactggaattgaagaacaaccactgtgagccatttgaactggtcatctccagaacc	843
QY	884	AACCTGTCAATGATTTCAGTGTGAGCCTCTATACAGACCAAGATTGGGATCATTAATG	943
Db	844	aacctgtcaatgtattcaagtgtagcctctcatacagacagattctgggattcatgaaactg	903
QY	944	TAGCATTCCCCGTGCGCAGCTTCAGCTTACTCTGTGATGTACTTCATTCACTGCTCGAAGG	1003
Db	904	tagcattccccctgycgcagcttcaagcttcaactctgaaigtacatccatctgcgaagg	963
QY	1004	AACGTAGTTAAATTGGGAAGAGAAACCAATTTGTGATGATCTGGAAATCTGGTCAATCC	1063
Db	964	aactgtagttaatttgggaagaagaagaacaacttgtgatacatctgtaacttgcataacc	1023
QY	1064	TAGTCCAAATATGTCAAAAATTGACAAAAGTTTCTCAATGATTAAAGAGGATTAATTA	1123
Db	1024	tagtccaataatgtaaaaaatttgacaagaattctccaatgataagaggygtatataaa	1083
QY	1124	CCCCCTGTATCTTCCACTGGCAGTCAGTACTGTGATCTCTGGTGGCGATTATATAT	1183
Db	1084	cccccttctaattccagctggcagctcatgltactgtaattctcttggcttggcaattatcat	1143
QY	1184	TTTGCTGTGCAAGGAGATTAAAAAAAGGCAAGAATCAAGAGAAATATGAATGACCCATA	1243
Db	1144	tttgctgtgcaaggyaggtttaaaaaaagycaaagaatccaagagaatataatgatacccta	1203
QY	1244	TTTAAATGCCCCCTTGGTGAAGAAATTTCTTGAATATCTTAAATCATGAGATCTTTTAA	1303
Db	1204	tttaaatgccttctgtgaagaanaattcttgyataactaanaatcatgataccctttaa	1263
QY	1304	TCCCTTCATGAAGCTTTTGTGTGTGGTGGCACCTCCCTACGTCAAAATGAAGTGTG-TTCC	1362
Db	1264	tcccttccaatgaagaattcttgtgtgtgagccctcccaagctcaaaaatgaagtggtttcc	1323
QY	1363	TTTCAGTGCATGTGGGAGAGATTTCCTACCCGACCAACAGTTCTTCACGTCTCCATTTCCGCC	1422
Db	1324	tttcagtgatcttgggaagaatttctacctgaaccaagaagcttccctcaagcttccattcgcc	1383
QY	1423	CTCATTTATCCCTTCACCCCCAGCCCAAGAGTGTATTATACAGCTCAGCTTTTGTCTTTT	1482
Db	1384	ctcatattacccctccaacccccagcccaagtggttatacagctcagcttttgccttt	1443
QY	1483	CTGAGGAGAAACAAATTAAGACAT-TAAGGAAAGATTTATGTGAAATTAAGATGGCT	1541
Db	1444	cttgaggagaaacaaataaagccataaaggyaaagatltcaatgtgaaatataaagaattgct	1503
QY	1542	GACTTGTGCTTTTCTTACACTCTGTTTTCAGTTCAATTCAGTGCCTGACCTTGAGATGAGAG	1601
Db	1504	gaacttgccttcttctgaactcctgttctcaagttcaatccaagtgctgaacttgatgaag	1563
QY	1602	ACACTTCTAAATGAAGTCAAAATTTGATACATATGTGAATATGAGCTCAGTTTCTTGCA	1661
Db	1564	acacttctaaatgagagcaaatltgatacataatggaatatgagctcgaatttcttgcga	1623
QY	1662	GATCAAAATTTACGTGCTCTTCTGTATCTGTGTGGAGGTCACTCTTATTAAGAAAGTTCAA	1721
Db	1624	gatacaaatltcaagctgtcttctgtatactgtgtgagtaacactctataagaagaattccaa	1683

Oy	1722	AAGTCTACGCTCTCTTTTCTTTTCTTAAGTCACAGTAGAAGTAAATGGGGTCCGTGCACAGTTGA	1781
Dd	1684	aagttcaagcttccttcttcttctaactccagaatgaattggygtcctgcctcaagttyga	1743
Oy	1782	AAGAATTCTATTTCACAGTGTAAGCCTCGCTGTGTAATAATTGGACATGCCATTTAACTGG	1841
Dd	1744	aagaatcccatcttgacagtagacctcgctcgctgtaattggaaatcctatacttaaccgg	1803
Oy	1842	CTTCAGGGCCCTCCCCACGCTTTCTTCAGCCACCCTCTCTTTTTCAAGTTGGCTGACTTCCACACC	1901
Dd	1804	cctca-gcctcccacactctctcaagcacactctcttcttcagttgctgcagctccaacc	1862
Oy	1902	TAGCATCTCATGAGTGGCCAGAACAAAAGAGAGAGAGAAATAGCCTGCGGGTTTTTTT	1961
Dd	1863	tagcatctccatagtagtgcacaagaagaagagaagaagaataagacbtgcgtgttltt	1922
Oy	1962	AGTTGGGGGGTTTTGGCGTGTTCCTTTATGAGACCCATTCGATTTCTTATATGACAATGT	2021
Dd	1923	agttgggggggtttgcgttcttcccttaabgaagccccatctcattctataagtaaacgt	1982
Oy	2022	TTCTTTTATCACGATATTATTATTAGTAAGAAACAATCACTGAATAATGCTAGCTGCAAGTGACA	2081
Dd	1983	tctcttatccagatatattatagtaagaanaactccactgaaatgtcagtcgcaagtgcaca	2042
Oy	2082	TCCTCTTGATGTCAATATGAGAAGATTAAAAACAGTGGAGAAATTCCTTGATTCAACATGA	2141
Dd	2043	tctcttgtatgatatalagaaagattaaaacagtcgagaagaattcccttgattccaagtga	2102
Oy	2142	AATGCTCTTCCTTTCCCTGCGCCGACAGACTTTTATCC-ACCTTACTAGATTCTACATATT	2200
Dd	2103	aatgctcttccttccctgcctgcccaagaccttatactcgaacttacagattctacatt	2162
Oy	2201	CTTTAAATTTTCATCTCAAGGCTCGCTCCCTCAACCCCAC	2265
Dd	2163	ccttaaattcatactcagcgtccctccaaccacc	2197
RESULT 13			
AAQ21184			
ID	AAQ21184	standard; DNA; 2350 BP.	
XX	XX		
AC	AAQ21184;		
XX	XX		
Df	21-MAY-1992 (first entry)		
XX	XX		
DE	Encodes T lymphocyte-specific Leu8 Antigen major form.		
XX	XX		
KW	Rapid immunoselection cloning technique; cell surface antigen;		
KM	homng receptor; antigen-presenting cells; ss.		
OS	Homo sapiens.		
XX	XX		
FH	Key	Location/Qualifiers	
FT	CDS	50..1207	
XX	XX	/*tag= a	
PN	WO9201049-A.		
XX	XX		
PD	23-JAN-1992.		
XX	XX		
PF	15-JUL-1990; 90MO-USO4986.		
XX	XX		
PR	13-JUL-1990; 90US-0553759.		
PA	(GEHO-) GEN HOSPITAL CORP.		
XX	XX		
PI	Seed B, Aruffo A, Amiot M;		
DR	WPI. 1992-056864/07.		
XX	P-PADB; AAR20815.		
PT	New CD53 cell surface antigen and DNA encoding it - for		
PR	immuno-therapy and diagnosis of haematopoietic neoplasms, etc.		

XX Example 14; Page 106; 160pp; English.

PS Two cDNA clones encoding Leu8 determinants were isolated from a
CC human T cell library using the rapid immunoselection cloning method
CC (see e.g. AAO21164 for description of method). The shorter insert
CC (see AAO22500) lacks 436 internal residues (i.e. nucleotides 1079 to
CC 1514 of the longer insert). RNA blot hybridisation
CC revealed a major transcript of 2.4kb in peripheral blood
CC mononuclear cells, tonsillar B cells and the Jurkat and HSB-2
CC leukemic T cell lines. A minor transcript of 2.0kb was present in
CC peripheral blood mononuclear cells and the Jurkat and HSB-2
CC leukemic T cell lines. The protein encoded by the larger insert
CC is closely related to the murine Mel-14 homing receptor.

SO Sequence 2350 BP; 679 A; 519 C; 490 G; 662 T; 0 other;

Query Match 94.1%; Score 2126.2; DB 13; Length 2350;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 2178; Conservative 0; Mismatches 13; Indels 4; Gaps 4;

QY 44 CCGTTGGCAGAGACCTGGAACCCCTGTGCTAAGTCAAGGCTCAATGGCTGCAGAG 103
DB 4 ccttctggcaaggacctgagacctctgtgctaaagcaaggctcaatggtctgcagaa 63
QY 104 AACTAGAGAGACCAAGCAAGCCATGATATTTCCATGGAATGTCCAGACCCAGAG 163
DB 64 aactagaagaagaccagaagccatgatatctccatggaatgtcagaagccagag 123
QY 164 GGCATTATGAGACATCTTCAAGTTGGGGGTGAGCAATGCTGTTGATTTCCTGGC 223
DB 124 ggcattatggaacatctcaagctgtggtggtgagcaatgctgtgtgatttcttgc 183
QY 224 AACTCATGGAACCTACTGCTGAGCTTACCATTTATCTGAAAAACCATGAACTGCGAAG 283
DB 184 aactcatggaacccgactgagctgtgactacatctatctgaaaaacccatgaactggaag 243
QY 284 GGGCTAGAAATTTCTGCCGAGACAAATTACACAGATTAGTTGCCATCAAAACAGCGGA 343
DB 244 gggctagaagattctgcgcgagacatcaacagattagttgcatacaaaacagcgga 303
QY 344 AATTGATTTCTGGAGAGACTCTGCCCTTCAAGTCTTACTACTGATAGGAATCCG 403
DB 304 aattgattctcggagaagactctgccttcaagctgtcttactactgtaggaatccg 363
QY 404 GAGATAGAGAGAAATGTGACGCGGTGGGAGCAACAATCTCTCAGCAAGAGCAAA 463
DB 364 gaagataagagaataatgagcgtggtggtggaaccaaacaatctcactgaagaacaga 423
QY 464 GAAGTGGGAGATGAGTGAAGCCCAACAAGAAAGAAACAAGAGAGACTGCGTGAATCTA 523
DB 424 gaactgggagatgtgtgagcccaacaagaagaacaaagggactgctgtgagatcca 483
QY 524 TATCAAGAGAAACAAAGATGACAGCAAAATGGAACGATGACGCTGCCACAACTAAGGC 583
DB 484 tatcaagagaacaagaatgacagcaaatggaagatgacgcctgccacaactaaaggc 543
QY 584 ACCCCCTGTGTACAGCTTCTTGGCAGCCCTGTCATGCAATGGCCATGGAGATGTGT 643
DB 544 accccctgtgtacacagcttcttgcagccctgtcattcagtgccatgaggaatgtgt 603
QY 644 AGAAATCATCAATTAATCAACACTGCAAGCTGTGATGTGGGGTACTATGGGCCCACTGCA 703
DB 604 agaatacatcaataatcaactgcaactgtgattgtggtgtactcttggcccccaatgtca 663
QY 704 GCTTGTGATTCAGTGTGAGCTTTGGAGGCCCCAGAGCTGGGTACCATGAGACTGACTCA 763
DB 664 gcttgtgattcagtgtagccttggagggcccccagagctgtgtaccatgagctgtactca 723
QY 764 CCGCTTTGGAACCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 823
DB 724 cctcttgggaactcagctcagctcagctcagctcagctcagctcagctcagctcagctcag 783

QY 824 CTTAACTGGGATTGAAGAAACCACTGTGGACCACTTTGGAAACTGCTATCTCCAGAAC 883
DB 784 ctttaactgggattggaagaaacccacctgtgaccatttggaaactgtcattccagaacc 843
QY 884 AACCTGCAAGTATTCAGTGTGAGGCTCTATCAGACACAGATTGGGGATCATGAACG 943
DB 844 aacctgcaagtattcagtgtagcctctcaacagacacagatttgggatacagaactg 903
QY 944 TAACCATCCCTGGCCAGCTTACGTTTACCTGTCATGCTTACCTGCTGCAAGG 1003
DB 904 taaccatccctggccagcttcaagcttcaactcctgatttactcattcattcgtcgaag 963
QY 1004 AACTGATTAATTTGGGAAAGAAACCAATTTGTGATATCATGTGAATGCTCAATTC 1063
DB 964 aactgattaatgtggaagaagaacacattgtgatactatctggaatctgttcaaatcc 1023
QY 1064 TAGTCCATATGTCAAAATTAATTTGACAAAAGTTTTCATGATTAAGAGGGATTTATTA 1123
DB 1024 tagtccaatatgttcaaaaatttggacaaaagtttccaatgattaagggatgtattataa 1083
QY 1124 CCGCTCTTCATTCAGTGTGACAGTCAATGCTTACCTGCTGCTGCAATTTATCAT 1183
DB 1084 cccgcttctcattccagtgtagcagctatgttactgattcctctgtgtggaattatcat 1143
QY 1184 TTGGCTGGCAGAGAGATTAAAGGCAAGAAATCCAAAGAAATGATATGATGACCCATA 1243
DB 1144 ttggctggcagagagattaaaagggcaagaaatccaaagaaaglatgaaatgaccata 1203
QY 1244 TTAATGCGCCCTTGGTGAAGAAATTTCTGGAATTAATAAATCATGATGATCTTTTAA 1303
DB 1204 ttaatgccccttggtagaagaataatcttgaataactcaaaaatcatatgagatcccttaa 1263
QY 1304 TCCCTTCATGAAGACGTTTGTGTGTGGACCTCTTACGTCAACATGAAAGTGTG-TTCC 1362
DB 1264 tcccttcatagaacagcttgtgtgtgtgacccctcctcagctcaaaacatgaagtgttcc 1323
QY 1363 TTCAGTGACCTGGGAGAGTTTCTACCGGACCAACAGTTCTTCAAGTTCCATTTCGCCC 1422
DB 1324 ttcaagtacatcgtggaagaattcttcaaccgacaagttccctcagcttccatttgcgcc 1383
QY 1423 CTCATTTATCCCTCAACCCCGCCAGCCAGAGTGTATTAACAGCTCAGCTTTTCTTTT 1482
DB 1384 ctcatattccctcaaccccgccagagtggttataacgctcagcttcttcttctt 1443
QY 1483 CTGAGAGAAACAAATTAAGACCAT-AAAGGAAAGGATTCAATGGAATTAAGAGGCT 1541
DB 1444 ctgagagaagaacaataagacacataaagggaagatcatctgtgaaatataaagatgct 1503
QY 1542 GACTTGTCTTTCTTGTGACTCTGTGTTTCAATTCATTCAGTGTGCTGATGATGACAG 1601
DB 1504 gacttgtcttcttctgtgactctgttctcaagttcaactcagtgctgtaacttgaagcag 1563
QY 1602 ACACCTTCAATTAAGAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1661
DB 1564 acaacttcaaatgaagtgcaaatattgataacatgataatgacacccagtttcttgca 1623
QY 1662 GATCAAAATTTACAGTCTGTTCTGTATTAAGTGTGAGGATCACTTTATTAAGAGTCAAA 1721
DB 1624 gatcaaaatttcaagctgtcttctgtatattgtggaaggtacaccttataagaagttcaaa 1683
QY 1722 AAGTCTACGCTCTCTTCTTCTTCACTCAAGTGAATGAGGAGTCTGCTCAAGTTGA 1781
DB 1684 aagctctacgctctcttcttcttcaactccagtgaaatgaatgggtctcgtccaaagtga 1743
QY 1782 AAGAGTCTAATTTACAGTGTGAGCTGCGCTGTGTGATTAAGAGTCAATCAATTAATTA 1841
DB 1744 aagagtcattatgttcaactgttagcctcgctgtgtgattggaaatccatttaacttg 1803
QY 1842 CTTAAGGCTCTCCACCTCTTCTTCAAGCCACCTCTCTTTTATGTTGGTGAATTCACACC 1901
DB 1804 cttaagctctccacctcttctcagccacactcttcttcaagttgtgtgtgtgtgtgtgtgt 1862

[illegible]

CC the isolation and molecular cloning of any protein which can be
CC expressed and transported to the cell surface membrane of a
CC eukaryotic cell. It has been used to clone genes (see AAB1198-220)
CC encoding cell surface antigens such as CD1a, CD1b, CD1c, CD6,
CC CD7, CD13, CD14, CD16, CD19, CD20, CD26, CD27, CD28, CD31,
CC CDW32a, CDW32b, CD33, CD34, CD36, CD37, CD38, CD39, CD40, CD43,
CC CD44, CD53, ICAM, LFA-3, FcR1a, FcR1b, T11sa and Leu8 (see
CC AAB6188-62, AAB8151-52 and AAB8151). CD40 cDNA (see AAB81198) is
CC specifically claimed. Leu8, a T lymphocyte antigen, has been
CC expressed in COS cells.
XX
SQ Sequence 2350 BP; 679 A; 521 C; 489 G; 661 T; 0 other;

Query Match 94.1%; Score 2126.2; DB 20; Length 2350;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 2178; Conservative 0; Mismatches 13; Indels 4; Gaps 4;

QY 44 CCGTTGGCAAGGACCGGAGACCGCTGTGCTAAGTCAAGAGGCGTCATGGGCTGCAGAAAG 103
DB 4 cccctggcagaagaccctgagaccctgctgaagtcagaagggctcaatggctgcagag 63

QY 104 AACTAGAGAGGACCAAGCAAGCCATGATGATTTCCATGGAATGTTCAGACGCCAG 163
DB 64 aactagagaagagcagaagcagaatgatattccatggaaatgttcagagccagag 123

QY 164 GGCATTATGGAACATCTTCAAGTTGTGGGGGTGACAAATCCTGTTGTGATTTCTGGC 223
DB 124 ggcattatggaaacatcttcaagttgtgggggtgacaatcctgttgtatctccggc 183

QY 224 ACATCATGGAACCTACGCTGCGGACTTACCATTTCTGAAAGCCCAAGCAAGCGCAAG 283
DB 184 acatcatggaaacctacgctgcggaacttaccatcttcgaaacccaagcaagcgaaag 243

QY 284 GCGTAGAAGATTTGCGCGAGACATTTACAGATTTAGTGGCATAAAGAGCGGA 343
DB 244 gcgtagaagatttgcgcgagacatttacagatttcagtcacataaagaagggga 303

QY 344 AATTGATATCTGGAGAGACCTGCGCTTCACTGTTTACTGATAGGAATCG 403
DB 304 aattgatattctggagagacctgccttcaagtcgttctactactggaagaatcgg 363

QY 404 GAAGATAGGAGGAAATATGAGCGTGGGGGAGCAACCAATCTCTCTCAAGAGAGAGA 463
DB 364 gaagataggaggaatattgagcgtgggagaccaaactctctcaagaaagaaga 423

QY 464 GAACGTGGGAGATGTGAGCGCCAAACAAGAACAAAGAGGACTGCTGGAGATCTA 523
DB 424 gaactggggagatgtgagcgccaaacaagaagaagaaggaactgcgtggagatcta 483

QY 524 TATCAAGAGAAACAAGATGCAAGCAATGGAAGATGACGCTGCCAACAATAAGGC 583
DB 484 tatcaagagaaacaagaatgcaagcaatggaacgactgcgcacaacaataaagc 543

QY 584 AGGCGCTGTATACAGCTCTTGGCCAGCCCTGTCATGAGAGTGGCCATGAGAAATGCT 643
DB 544 aggcgctgttatcacagctcttgcagcccggtgcatacgaatggccaatgaatgtgt 603

QY 644 AGAATCATCAATTAATACACGTCAACTGTGATGGGGTACTATAGGGCCCAAGTTCA 703
DB 604 agaatcatcaatataataacacgtcaactgtgtgtgggtactatagggcccaagtgtca 663

QY 704 GCTTGTGATTTCACTGTGAGCGCTTTGGAGCGCCAGAGCTGGGTACCATGAGCTGTACTCA 763
DB 664 gcttgtgatcttcaactgtgagcgcttggagcgccagagctggatcaatggactgtca 723

QY 764 CCGCTTTGGAAACTTTCAGCTTCAGCTCACAGTGTGCTTACGCTGCTCTAAGAACAAA 823
DB 724 cctcttggaaaacttctcagcttcacagatgtgcttcaagctgtcttgaagaaacaaa 783

QY 824 CTTAATCTGGATTTGAAGAAACACACTGTGAGCAATTTGAAATGTCATCTCCAGAAC 883
DB 784 cttaactggatgtgaagaaacacactgtggaccaatttgaaactgttcatctccagaacc 843

QY 884 AACCTGCAAGTGTATAGTGTGAGCTCTATACGACCAAGATTTGGGATCATGAACCTG 943
DB 844 aacctgcaagtgatataagtgtagccctctatacagcacagatctgggatacgaactg 903

QY 944 TAGCAATCCCTGGCCGAGCTTACGCTTACCTCGATGTAACCTTCAATCGCTCAGAAAG 1003
DB 904 tagcaatccctggccgagcttcaagcttaccctcgcaatgcacctcactcgctcagaag 963

QY 1004 AACTGATTAATTGGGAAGAAAGAAACCAATTTGTAATCATCTTGGAATCTGTCAAAATCC 1063
DB 964 aactgattaatgggaagaaagaaacacatttggaaatcatctggaatctcgtaaatcc 1023

QY 1064 TAGTCCAAATATGCAAAAATTTGGCAAAAGTTTCTCATATGTTAAGAGGCTGATTTAA 1123
DB 1024 tagtccaatattgtaaaaaattggacaaaagtttctcaatgataaggaaggtagattaa 1083

QY 1124 CCGCCTCTTCAATTCAGTGGCAGTCATGATGTTACTGCTTCCTGCTGGTGGCATTATCAT 1183
DB 1084 cgcctctcaatctcagtggcagatcagtgatctacgtctctcgggttgacattatcatc 1143

QY 1184 TTGGCTGGCAAGAGATTTAAAAAAGCAAGAAATCCAGAGAAATGATGACCCATA 1243
DB 1144 ttggctggcaagagatataaaaaaggcaagaaatccaagagaagtagaagaccata 1203

QY 1244 TTAATGCGCCTTGTGTAAGAAATTTCTTGGAATTAATAAATCATGACATCCTTTAAA 1303
DB 1204 ttaatgccccttgtgtaagaaatcttggaaatacctaataatcagaatccctttaa 1263

QY 1304 TTCTTCATGAAGCGTTTGTGTGTGGGCAACCTCTGCAAAACATGAAGTGTG-TTCC 1362
DB 1264 tcttccatgaagcgttctgtgtgtgggcaacctctgcaaaaacatgaagtgtctcc 1323

QY 1363 TTGAGTCATCTGGGAGGATTTTACCCGACCAACAGTTCTTTCAGCTTCATTTCCGCC 1422
DB 1324 ttgagtcacttgggaagatttctacctgacaaacagttctctcaagttccattcgcc 1383

QY 1423 CTCATTTATCCCTACACCCCGACCCAGAGTGTTTATACAGCTCAGCTTTTGTCTTTT 1482
DB 1384 ctcatattatcccttaaaccccgacagccagtggttataagctcagcttcttcttct 1443

QY 1483 CTGAGGAGAAACAAATTAAGCCAT-AAAGGAAAGATTCATGTGGATTAAGATGCGT 1541
DB 1444 ctgaggaagaaacaataagaccataaaggaaagatctcagaaataaagaatggc 1503

QY 1542 GACTTTCCTTCTTGTGACCTTGTGTTTCAATTCAGTCTGCTTGTGATGACAG 1601
DB 1504 gaacttgccttcttcttgacctctgtttcagtttcaatcagtcagtcgttactgtgacg 1563

QY 1602 ACACCTTAATGAAGTGAATTTGTATACATATGTAATGACATGACTTTTCTTGCA 1661
DB 1564 acactttaaattgaagtgcaaatltgatacalgtgaaatlgaaacccagtttcttgca 1623

QY 1662 GATCAATTTACAGTGTGCTCTGTTGTAATGAGTGTGAGTGTATGAAAGTTCAA 1721
DB 1624 gatcaaatttacagtgctcttctgtaacgtggaagtgaaacccataagaagaatcaa 1683

QY 1722 AAGTCTACGCTCTCTTCTTCTTCACTCAAGTGAATTAATGGGGTCTGCTCAAGTTGA 1781
DB 1684 aagtctacgctctctcttcttctcaactccagtgaaatgaatgggtctgctcaagttga 1743

QY 1782 AAGAGTCTATTGTGACATGTAGCCTGCGCGTCTGTGAATTTGACCAATCTATTAACTGG 1841
DB 1744 aagaagctctatttgcaacttgagctcgcgctcgttgatattgaaacccataatlaactgg 1803

QY 1842 CTTGAGGCGTCCCGACCTCTGTCAGCCACCTCTTTTGTAGTTGGTGAATTCACAC 1901
DB 1804 ctcca-gcctccccaactcttccagccaactcttcttcaagttgagcttccacaacc 1862

QY 1902 TACCATCTCATGAGTGTGCAAGAAAGAGAGAGAGAGAAATGAGCTGCGCGGTTTTTT 1961
DB 1863 tagcatctcatgtgtgcaagcaaaaggagaagagagaatacagctcgctgcttcttct 1922

QY 1962 AGTTGGGGGTTTTCGTGTTTCTTTAAGAGACCCATTCCPATTTCTTATAGTCATGT 2021
Db 1923 agttggggggttttgcgttttcccttatgagaccattcctattcttatagtaatgt 1982
QY 2022 TTTCTTTATCAGATATTTATAGTAAAGACATCATGAATGCTAGCTGCAAGTGACA 2081
Db 1983 ttctttatcacgatatattagtaagaaacatcactgaatgctagctgcaagtgaca 2042
QY 2082 TCTCTTTGATGTCATATGAGAGTAAACAGTGAAGAAATTCCTTGATTCAATGA 2141
Db 2043 tctctttgatgacataagaaagatlaaacaagtcgagaaatccttgattcacaaatga 2102
QY 2142 AATGCTTCCTTCCCTGCCCCCAGAACCTTTATGC-ACCTAGTAGATCTACATATT 2200
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QY 2201 CTTTAATTTCAATCTCAGGCTCCCTCAACCCAC 2235
Db 2163 cttaaatlcatlcaagcctccctcaacccac 2197

Search completed: October 13, 2001, 01:44:50
Job time: 6945 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2001, 23:57:46 ; Search time 80.31 Seconds
(without alignments)
5325.038 Million cell updates/sec

Title: US-09-119-209-1

Perfect score: 2259

Sequence: 1 GAATTCGACAGTGTGCTGCTT.....CCGCCACACACTGGAATTC 2259

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 segs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents, NA:*

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- 2: /cgml_7/ptodata/1/lna/5B.COMB.seq:*
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- 6: /cgml_7/ptodata/1/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2259	100.0	2259	2	US-08-513-278-1
2	2087.6	92.4	2330	1	US-08-481-803-1
3	2087.6	92.4	2330	1	US-08-215-366A-1
4	2087.6	92.4	2330	1	US-08-340-539A-1
5	2087.6	92.4	2330	2	US-08-461-592B-1
6	1469.2	65.0	1829	6	5514582-1
7	922.2	40.8	1696	1	US-08-340-539A-11
8	922.2	40.8	1696	2	US-08-461-592B-11
9	856.8	37.9	2214	2	US-08-513-278-3
10	856.8	37.9	2214	6	5514582-3
11	385.2	17.1	531	1	US-08-340-539A-5
12	385.2	17.1	531	2	US-08-461-592B-5
13	310	13.7	1833	1	US-08-365-470-2
14	310	13.7	3834	3	US-09-209-668-18
15	310	13.7	3854	1	US-08-365-470-1
16	310	13.7	3858	2	US-08-344-155C-98
17	310	13.7	3863	6	5217870-1
18	294.8	13.1	3142	1	US-08-110-158-3
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20	240.2	10.6	2989	6	5378464-1
21	223.4	9.9	1592	2	US-08-252-493C-1
22	223.4	9.9	1592	3	US-09-276-197-1
23	189.4	8.4	451	1	US-08-340-539A-8
24	189.4	8.4	451	2	US-08-461-592B-8
25	183.8	8.1	712	1	US-08-340-539A-7
26	183.8	8.1	712	2	US-08-461-592B-7
27	131.2	5.8	544	1	US-08-340-539A-9

28	131.2	5.8	544	2	US-08-461-592B-9	Sequence 9, Appl1
29	107.2	4.7	832	1	US-08-340-539A-6	Sequence 6, Appl1
30	107.2	4.7	832	2	US-08-461-592B-6	Sequence 6, Appl1
31	96.4	4.3	1192	1	US-08-340-539A-3	Sequence 3, Appl1
32	96.4	4.3	1192	2	US-08-461-592B-3	Sequence 3, Appl1
33	84.2	3.7	363	1	US-08-340-539A-4	Sequence 4, Appl1
34	84.2	3.7	363	2	US-08-461-592B-4	Sequence 4, Appl1
35	57.6	2.5	7218	1	US-08-232-463-14	Sequence 14, Appl1
36	47.4	2.1	7218	1	US-08-232-463-14	Sequence 14, Appl1
37	37	1.6	1430	1	US-08-276-452A-25	Sequence 25, Appl1
38	37	1.6	1430	2	US-08-798-744-25	Sequence 25, Appl1
39	37	1.6	5852	1	US-07-867-106-2	Sequence 2, Appl1
40	35.8	1.6	1179	2	US-08-465-794-4	Sequence 4, Appl1
41	35.8	1.6	1179	3	US-09-049-813-4	Sequence 4, Appl1
42	33.6	1.5	1700	2	US-08-897-340-4	Sequence 4, Appl1
43	33.6	1.5	1700	3	US-09-252-329-4	Sequence 4, Appl1
44	33.6	1.5	543	4	US-09-117-257-18	Sequence 18, Appl1
45	33	1.5	543	4	US-08-945-476-18	Sequence 18, Appl1

ALIGNMENTS

RESULT 1
Sequence 1, Application US/08513278
Patent No. 5840844
GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: YEDNICK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,278
FILING DATE: 10-AUG-1995
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059027
FILING DATE: 06-MAY-1993
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
APPLICATION DATA:
APPLICATION NUMBER: 07/315015
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 565D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2259 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-513-278-1

Query Match	100.0%;	Score 2259;	DB 2;	Length 2259;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2259;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	GAATTCAGTGTCTGGCTTCTCTCACTCTGACACACAGCACACTCCCTTTGGACAGACT	60
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QY	61	GAGACCCCTTGTGTAGTCAAGAGGCTCAATGGGTGCAGAAAGAACTAGAGAGGACCA	120
Db	61	GAGACCCCTTGTGTAGTCAAGAGGCTCAATGGGTGCAGAAAGAACTAGAGAGACCA	120
QY	121	GCAAAGCCATGATATTTCCATGGAAATGTCAAGACCCAGAGGGACTTATGAAATCT	180
Db	121	GCAAAGCCATGATATTTCCATGGAAATGTCAAGACCCAGAGGGACTTATGAAATCT	180
QY	181	TCAAAGTGTGGGGGAGGACAAATGCTCTGTGGATTTCTGTGGCAATCATAGAAACCTACT	240
Db	181	TCAAAGTGTGGGGGAGGACAAATGCTCTGTGTGGATTTCTGTGGCAATCATAGAAACCTACT	240
QY	241	GCTGGACTTACATTAATTTCTGAAAAAACCATGAACTGGCAAAAGGGCTAGAAAGATTCTGCC	300
Db	241	GCTGGACTTACATTAATTTCTGAAAAAACCATGAACTGGCAAAAGGGCTAGAAAGATTCTGCC	300
QY	301	GAGACATATTACACATATTAGTGTGCATCAAAAAAAGGGGGAAATAGATACTGGACA	360
Db	301	GAGACATATTACACATATTAGTGTGCATCAAAAAAAGGGGGAAATAGATACTGGACA	360
QY	361	AGACTGTGCCCTTCACTGCTCTTACTACTGATAGGAATCCGGAAGATAGAGGAATAT	420
Db	361	AGACTGTGCCCTTCACTGCTCTTACTACTGATAGGAATCCGGAAGATAGAGGAATAT	420
QY	421	GGACGTGGGTGGGAACCAAAATCTCTCACTGTAAGAAAGCAGAGAACTGGGGAGATGTG	480
Db	421	GGACGTGGGTGGGAACCAAAATCTCTCACTGTAAGAAAGCAGAGAACTGGGGAGATGTG	480
QY	481	AGCCCAACACAGAAGAAACAGAGAGACTGCGTGAGACTTATATCAAGAGAAACAAG	540
Db	481	AGCCCAACACAGAAGAAACAGAGAGACTGCGTGAGACTTATATCAAGAGAAACAAG	540
QY	541	ATGCAAGGCAATGGAAGCATGACCCCTGCGACAAACTTAAAGGACGCCCTGTGTACACAG	600
Db	541	ATGCAAGGCAATGGAAGCATGACCCCTGCGACAAACTTAAAGGACGCCCTGTGTACACAG	600
QY	601	CTTCTTGCAGCCCTGTGTCATGACAGTGGCCATGGAAGATGTGTAGAAATCATCAATTAATC	660
Db	601	CTTCTTGCAGCCCTGTGTCATGACAGTGGCCATGGAAGATGTGTAGAAATCATCAATTAATC	660
QY	661	ACACTGTCAACTGTGATGTGGGGTACTATATGAGGCCCAAGTGTCAAGTTGTGATTCAGTGTG	720
Db	661	ACACTGTCAACTGTGATGTGGGGTACTATATGAGGCCCAAGTGTCAAGTTGTGATTCAGTGTG	720
QY	721	AGCCTTTGAGAGGCCCAAGAGCTGGGTGCATATGAGACTGTACTACCCCTTTGAAACTTCA	780
Db	721	AGCCTTTGAGAGGCCCAAGAGCTGGGTGCATATGAGACTGTACTACCCCTTTGAAACTTCA	780
QY	781	GCTTCAGCTCACTGTGTCCCTTCAAGCTGCTCTGAAAGAACTTAACGTGGATTGAAG	840
Db	781	GCTTCAGCTCACTGTGTCCCTTCAAGCTGCTCTGAAAGAACTTAACGTGGATTGAAG	840
QY	841	AAACACACTGTGGACCAATTTGAAACCTGGTGCATCTCCACAACCAACCTGTCAAGATTC	900
Db	841	AAACACACTGTGGACCAATTTGAAACCTGGTGCATCTCCACAACCAACCTGTCAAGATTC	900
QY	901	AGTGTGAGCCTATATCAGCACACAGATTTGGGGATCATGAATGTAGGCATCCCTGGGCA	960
Db	901	AGTGTGAGCCTATATCAGCACACAGATTTGGGGATCATGAATGTAGGCATCCCTGGGCA	960
QY	961	GCTTCACCTTACTCTGCATGTACTTATCTCTCAGAAAGAACTAGTTAATTGGGA	1020
Db	961	GCTTCACCTTACTCTGCATGTACTTATCTCTCAGAAAGAACTAGTTAATTGGGA	1020

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Qy	1021	AGAGAGAAACCATTTGTGTGATCATCTGGAAATCTGGTCAAAATCCTAGTCCAAATATGTCAAA	1080
Db	1021	AGAGAGAAACCATTTGTGTGATCATCTGGAAATCTGGTCAAAATCCTAGTCCAAATATGTCAAA	1080
Qy	1081	AATTTGACAAAAGTTTTCATAGATTAAGAGGGGTGTTTAACCCCGCTTCATTCCAG	1140
Db	1081	AATTTGACAAAAGTTTTCATAGATTAAGAGGGGTGTTTAACCCCGCTTCATTCCAG	1140
Qy	1141	TGGCAGTCATGGTTACTGCATTTCTGGGTTTGGATTATCATTTTGGCTGGCAGCAAGAGAT	1200
Db	1141	TGGCAGTCATGGTTACTGCATTTCTGGGTTTGGATTATCATTTTGGCTGGCAGCAAGAGAT	1200
Qy	1201	TAAAAAAAGGCAAGAAATCCAGAGAAAGTATGATGATACCCATTTTAATGCGCTTGTGTG	1260
Db	1201	TAAAAAAAGGCAAGAAATCCAGAGAAAGTATGATGATACCCATTTTAATGCGCTTGTGTG	1260
Qy	1261	AAGAAGAAATCTTGGAAATCAATAAATCAATGATATCCTTTAAATCCTTCATGAAAGCTT	1320
Db	1261	AAGAAGAAATCTTGGAAATCAATAAATCAATGATATCCTTTAAATCCTTCATGAAAGCTT	1320
Qy	1321	TGTGTGTGTGTGACCTCCTACGTCAAAACATGAAGTGTGTTCTTAGTGATGTGTGGAG	1380
Db	1321	TGTGTGTGTGTGACCTCCTACGTCAAAACATGAAGTGTGTTCTTAGTGATGTGTGGAG	1380
Qy	1381	ATTTCACCCGACACAAAGTTCCTTCAGCTTCATTCGCCCCCTCATTTATCCGCAAC	1440
Db	1381	ATTTCACCCGACACAAAGTTCCTTCAGCTTCATTCGCCCCCTCATTTATCCGCTCAAC	1440
Qy	1441	CCGACGCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTTCTGAGAGAAACAAATTA	1500
Db	1441	CCGACGCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTCTGAGAGAAACAAATTA	1500
Qy	1501	GACCAATTAAGGGAAGAGATCATCTGTGGAAATTAAGATGGCTACATTCGCTTCTTGAC	1560
Db	1501	GACCAATTAAGGGAAGAGATCATCTGTGGAAATTAAGATGGCTACATTCGCTTCTTGAC	1560
Qy	1561	TCCTGTGTTTCAGTTTCAATTCAGTGTCTGATCTTGATGACAGACATTTAAATGAAGTGC	1620
Db	1561	TCCTGTGTTTCAGTTTCAATTCAGTGTCTGATCTTGATGACAGACATTTAAATGAAGTGC	1620
Qy	1621	AAATTTGATACATATGGAATATGAGATGAGATGAGTTTCTGAGATCAAAATTTCAAGTGTGC	1680
Db	1621	AAATTTGATACATATGGAATATGAGATGAGATGAGTTTCTGAGATCAAAATTTCAAGTGTGC	1680
Qy	1681	TTCTGTATATCTGTGAGGTACACTCTTATAGAAAGTCCAAAAGTCAACGTCCTCTTC	1740
Db	1681	TTCTGTATATCTGTGAGGTACACTCTTATAGAAAGTCCAAAAGTCAACGTCCTCTTC	1740
Qy	1741	TTTTCTAACTCCAGTGAAGTATGAGGTGCTGTCTCAAGTTGAAAGTCAATTTTGACATG	1800
Db	1741	TTTTCTAACTCCAGTGAAGTATGAGGTGCTGTCTCAAGTTGAAAGTCAATTTTGACATG	1800
Qy	1801	TAGCTGCGCGTCTGTGAATTTGAGCAATCTTATTAATCTGAGCTTCAGGCGTCCCAACTT	1860
Db	1801	TAGCTGCGCGTCTGTGAATTTGAGCAATCTTATTAATCTGAGCTTCAGGCGTCCCAACTT	1860
Qy	1861	CTTACAGCACCTCTCTTTTTCAGTTGGCTGACTTCCACACCTAGCATCTCATGAGTGCA	1920
Db	1861	CTTACAGCACCTCTCTTTTTCAGTTGGCTGACTTCCACACCTAGCATCTCATGAGTGCA	1920
Qy	1921	AGCAAAAGGAGAGAGAGAAATAGCCGCGCGGCTTTTATGTTTGGGGGTTCCTGT	1980
Db	1921	AGCAAAAGGAGAGAGAGAAATAGCCGCGCGGCTTTTATGTTTGGGGGTTCCTGT	1980
Qy	1981	TTTCCTTTTATGAGACCATCTCATTTCTTATAGTCATGTTTCTTTTATACAGATATTA	2040
Db	1981	TTTCCTTTTATGAGACCATCTCATTTCTTATAGTCATGTTTCTTTTATACAGATATTA	2040
Qy	2041	TTTAGTAAAGAAACATCATGAAATCTTAGCTGACAGTGTACATCTCTTGATGTATATGG	2100
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QY 2101 AAGAGTTAAACAGTGTGAGAAATTCCTTGATTCACATGAATGCTCTCTTCCCTG 2160
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Db 2101 AAGAGTTAAACAGTGTGAGAAATTCCTTGATTCACATGAATGCTCTCTTCCCTG 2160
QY 2161 CCCCCAGAACTTTTATCAGCTTACTAGATTCACATATTTCTTAAATTCATCTCAGGC 2220
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Db 2161 CCCCCAGAACTTTTATCAGCTTACTAGATTCACATATTTCTTAAATTCATCTCAGGC 2220
QY 2221 CTCCTCAACCCCGAGGGGCGCCGACAGACATGGAATTC 2259
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Db 2221 CTCCTCAACCCCGAGGGGCGCCGACAGACATGGAATTC 2259
RESULT 2
US-08-481-803-1
; Sequence 1, Application US/08481803
; Patent No. 5679346
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F. and Olivier G. Sperlnt
; TITLE OF INVENTION: MONOCLONAL ANTIBODY TO LYMPHOCYTE-ASSOCIATED CELL
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,803
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,366
; FILING DATE: 21-MAR-1994
; APPLICATION NUMBER: US 07/720,602
; FILING DATE: 25-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/313,109
; FILING DATE: 21-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: CG-101 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 53..1210
; US-08-481-803-1

Very Match 92.4%; Score 2087.6; DB 1; Length 2330;
Local Similarity 98.5%; Pred. No. 0;
Ches 2161; Conservative 0; Mismatches 24; Indels 9; Gaps 5;

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Db 7 CCTTTGGGAGAGACCTGAGACCTCTGTGCTAAGTCAAGAGGCTCAATGGGCTGCAGAG 66
QY 104 AACTAGAGAGAGACCAAGCAAGCCATGATATTTCCATGGAATGTGCAGAGCCAGAG 163
| | | | |
Db 67 AACTAGAGAGAGACCAAGCAAGCCATGATATTTCCATGGAATGTGCAGAGCCAGAG 126
QY 164 GGAATTATGAGAACATCTTCAAGTTGTGGGGGTGAGCAATGCTGTGTGATTTCTGGC 223
| | | | |
Db 127 GGAATTATGAGAACATCTTCAAGTTGTGGGGGTGAGCAATGCTGTGTGATTTCTGGC 186
QY 224 ACATCATGAGAACTACTGCTGGACTTACCATTTTCTGAAAAACCATGAACTGGCAAG 283
| | | | |
Db 187 ACATCATGAGAACTACTGCTGGACTTACCATTTTCTGAAAAACCATGAACTGGCAAG 246
QY 284 GGCTAGAGATTTGCGCGAGACAAATTAACAGATTTAGTGGCATACAAAACAAGGCGGA 343
| | | | |
Db 247 GGCTAGAGATTTGCGCGAGACAAATTAACAGATTTAGTGGCATACAAAACAAGGCGGA 306
QY 344 AATTGATATCTGAGAGAAAGACTGCGCTTCACTGCTTCTTACTAGTGAATGCG 403
| | | | |
Db 307 AATTGATATCTGAGAGAAAGACTGCGCTTCACTGCTTCTTACTAGTGAATGCG 386
QY 404 GAAGATAGAGAGAAATATGAGCTGGGTGGGACCAACAATCTCTCACTGAGAGACAGA 463
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Db 367 GAAGATAGAGAGAAATATGAGCTGGGTGGGACCAACAATCTCTCACTGAGAGACAGA 426
QY 464 GAACGGGGAGATGATGAGCCCAACAAGAAACAAGAGAGACTGGGTGAGATCTA 523
| | | | |
Db 427 GAACGGGGAGATGATGAGCCCAACAAGAAACAAGAGAGACTGGGTGAGATCTA 486
QY 524 TATCAAGAGAAACAAGATGACAGCAAAATGGAAGATGAGAGCTGCGCACAAATAAGGC 583
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Db 487 TATCAAGAGAAACAAGATGACAGCAAAATGGAAGATGAGAGCTGCGCACAAATAAGGC 546
QY 584 AGCCCTGTGTACACAGCTTCTTGGCCAGCCCTGCTATGACAGTGGCCATGAGAAATGTGT 643
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Db 547 AGCCCTGTGTACACAGCTTCTTGGCCAGCCCTGCTATGACAGTGGCCATGAGAAATGTGT 606
QY 644 AGAAATCATCAATTAATACACACCTGCAACTGTGATGAGGGGTACTATGAGGCCCAAGTCTA 703
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Db 607 AGAAATCATCAATTAATACACACCTGCAACTGTGATGAGGGGTACTATGAGGCCCAAGTCTA 666
QY 704 GCTTGTGATTCAGTGTGAGGCTTTGGAGGCCCGAGAGCTGGGTACCATGAGACTGTACTCA 763
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Db 667 GCTTGTGATTCAGTGTGAGGCTTTGGAGGCCCGAGAGCTGGGTACCATGAGACTGTACTCA 726
QY 764 CCCCCTTGGAAACTTCAAGCTTCAAGCTCAGCTGAGTGGCTTCACTGCTGAGAGAAACAA 823
| | | | |
Db 727 CCCCCTTGGAAACTTCAAGCTTCAAGCTCAGCTGAGTGGCTTCACTGCTGAGAGAAACAA 786
QY 824 CTTAAGTGGATTAAGAAACCAACCTGTGAGACATTTGGAACCTGTGCATCTCCAGAAC 883
| | | | |
Db 787 CTTAAGTGGATTAAGAAACCAACCTGTGAGACATTTGGAACCTGTGCATCTCCAGAAC 846
QY 884 AACCTGTCAAGTATTCAGTGTGAGGCTGTATCAGCAGCAGATTTGGGATCTGAACCTG 943
| | | | |
Db 847 AACCTGTCAAGTATTCAGTGTGAGGCTGTATCAGCAGCAGATTTGGGATCTGAACCTG 906
QY 944 TAGCCATCCCTGCGCAGCTTCAAGCTTACCTGTGATGATGATGATGATGATGATGATG 1003
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Db 907 TAGCCATCCCTGCGCAGCTTCAAGCTTACCTGTGATGATGATGATGATGATGATGATG 966
QY 1004 AACTGATTAATTTGGAAGAGAAACCAATTTGTAATCATCTGGAATCTGGTCAATGTC 1063
| | | | |
Db 967 AACTGATTAATTTGGAAGAGAAACCAATTTGTAATCATCTGGAATCTGGTCAATGTC 1026
QY 1064 TAGTCCAAATATGCAAAAATTTGGCAAAAATTTCTCAATGATTAAGAGAGGTGATTAATA 1123
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Db 1027 TAGTCCAAATATGCAAAAATTTGGCAAAAATTTCTCAATGATTAAGAGAGGTGATTAATA 1086

OY	224	ACATCATGGAACTCACTGCTGGACTTACCATTTATTTCTGAAAAACCATACTGGCAAG	283
Db	187	ACATCATGGAACTCACTGCTGGACTTACCATTTATTTCTGAAAAACCATACTGGCAAG	246
OY	284	GGCTGGAAGATTCCTGGCAGACATTTACACAGATTTAGTTGGCATCAAAACAGCGGA	343
Db	247	GGCTGGAAGATTCCTGGCAGACATTTACACAGATTTAGTTGGCATCAAAACAGCGGA	306
OY	344	AATTGAGTATCTGAGAGAAGACTGCCCCCTTCACTGCTTCTTACTACTGGATGGAATCCG	403
Db	307	AATTGAGTATCTGAGAGAAGACTGCCCCCTTCACTGCTTCTTACTACTGGATGGAATCCG	366
OY	404	GAAGTATGGAGAGATPATGGACGTGGGGGGAACCAACAAATCTCTACAGAGAGACGA	463
Db	367	GAAGTATGGAGAGATPATGGACGTGGGGGGAACCAACAAATCTCTACAGAGAGACGA	426
OY	464	GAACTGGGAGATGCTGAGGCCCAACAACAAGAAAGAACAGAGAGACTGCTGAGATCTA	523
Db	427	GAACTGGGAGATGCTGAGGCCCAACAACAAGAAAGAACAGAGAGACTGCTGAGATCTA	486
OY	524	TATCAAGAGAAACAAGATGCAAGCAAAATGGAAACGATGACGCTGCGCACAACTAAAGC	583
Db	487	TATCAAGAGAAACAAGATGCAAGCAAAATGGAAACGATGACGCTGCGCACAACTAAAGC	546
OY	584	AGCCCTGTTTACACAGCTTCTTGCCAGCCCTGGTATACAGTGGCCATGAGAAATGTGT	643
Db	547	AGCCCTGTTTACACAGCTTCTTGCCAGCCCTGGTATACAGTGGCCATGAGAAATGTGT	606
OY	644	AGAAATCATCAATATACACACTGECACACTGTGATGTGGGATACTATGGCCCCAGTCTCA	703
Db	607	AGAAATCATCAATATATTAACACTGECACACTGTGATGTGGGATACTATGGCCCCAGTCTCA	666
OY	704	GCTTGATTTAGTGTAGTGAGGCTTTTGGAGGCCCAAGAGCTGGGGATACCATGAGACTGTACTCA	763
Db	667	GTTTGTGATTTAGTGTAGTGAGGCTTTTGGAGGCCCAAGAGCTGGGGATACCATGAGACTGTACTCA	726
OY	764	CCCCCTTGGAACTTTCAGCTTCAAGCTTCACAGTGTGCTTCACTGCTGCGTGAAGAAACAA	823
Db	727	CCCCCTTGGAACTTTCAGCTTCAACCTTCAACCTCACAGTGTGCTTCACTGCTGCGTGAAGAAACAA	786
OY	824	CTTAACTGGGATTTTAAACAAACACACTGTGGACCATTTGGAAACTGGTCAATCTCCAGAAC	883
Db	787	CTTAACTGGGATTTTAAACAAACACACTGTGGACCATTTGGAAACTGGTCAATCTCCAGAAC	846
OY	884	AACCTGTCANAGTGAATGAGTGTGAGGCTCTATCAGCACACAGATTTGGGAGATCATGAATG	943
Db	847	AACCTGTCANAGTGAATGAGTGTGAGGCTCTATCAGCACACAGATTTGGGAGATCATGAATG	906
OY	944	TAGCATTCCTCGGCCAGCTTTCAGCTTTACCTGTGCATGTACCTTCATCTGCTCAAGAG	1003
Db	907	TAGCATTCCTCGGCCAGCTTTCAGCTTTACCTGTGCATGTACCTTCATCTGCTCAAGAG	966
OY	1004	AACGTAGTTAATTGGGAAGAAAGAAACCATTTGTGAATCATCTGGAAATCTGTCACAAATCC	1063
Db	967	AACGTAGTTAATTGGGAAGAAAGAAACCATTTGTGAATCATCTGGAATCTGTCACAAATCC	1026
OY	1064	TAGTCCAAATATGTCAAAATTTGGACAAAGTTTCTCAATGATTTAAGAGAGGTGATTTATPA	1123
Db	1027	TAGTCCAAATATGTCAAAATTTGGACAAAGTTTCTCAATGATTTAAGAGAGGTGATTTATPA	1086
OY	1124	CCCCCTTCATTCCTCACTGGCAGTCATGGTTACTGCATTTCTCGGGTTGGCATTTATCAT	1183
Db	1087	CCCCCTTCATTCCTCACTGGCAGTCATGGTTACTGCATTTCTCGGGTTGGCATTTATCAT	1146
OY	1184	TTGGCTGGCAGAGATTTAAAAAAGGCAAGAAATCAAGAGAAAGTATGAATGACCCATA	1243
Db	1147	TTGGCTGGCAGAGATTTAAAAAAGGCAAGAAATCAAGAGAAAGTATGAATGACCCATA	1206
OY	1244	TTAAATGCCCCCTTGGTGAAGAAAAATTTCTTGGAAATCTAAAAATCATGAGATCTTTTAA	1303
Db	1207	TTAAATGCCCCCTTGGTGAAGAAAAATTTCTTGGAAATCTAAAAATCATGAGATCTTTTAA	1266

QY	1304	TCCTCCCATGAAGAGTTTGTGTGTGGACCTCCACGTGCAAAACATGAAGTGTG -TTCC	1352
QY	1304	TCCTCCCATGAAGAGTTTGTGTGTGGACCTCCACGTGCAAAACATGAAGTGTG -TTCC	1352
Db	1267	TCCTTCCTGAAGAGTTTGTGTGTGGACCTCCACGTGCAAAACATGAAGTGTGTTC	1326
QY	1363	TTTCAGTGCATGTGGAGAGATTTTCACCCGCCAACAGTTCCTTCAGTCCATTTCCGCC	1422
Db	1327	TTTCAGTGCATGTGGAGAGATTTTCACCTGACCAACAGTTCTTCAGCTTTCATTTACCC	1386
QY	1423	CTCATTTTATCCCTCAACCCCCAGCCCAAGGTGTTTATACAGCTCAGCTTTTGTCTTTT	1482
Db	1387	CTCATTTTATCCCTCAACCCCCAGCCCAAGGTGTTTATACAGCTCAGCTTTTGTCTTTT	1446
QY	1483	CTGAGGAGAAACAATATAGACCAT -AAGGAGAAAGATTCATGTGGAATATATAAGTGGCT	1541
Db	1447	CTGAGGAGAAACAATATAGACCATATAAGGAGAAAGATTCATGTGGAATATATAAGTGGCT	1506
QY	1542	GACCTTGCTCTCTTTCTTGACACTTGTTTTCAGTTTCAGTTTCAGTGGCTGATCTTGATGACAG	1601
Db	1507	GACCTTGCTCTCTTTCTTGACACTTGTTTTCAGTTTCAGTTTCAGTGGCTGATCTTGATGACAG	1566
QY	1602	ACACTTCTAAATGAAGTGAATAATTTGATACATATGTGAATATGAGACTGAGTTTCTTGCA	1661
Db	1567	ACACTTCTAAATGAAGTGAATAATTTGATACATATGTGAATATGAGACTGAGTTTCTTGCA	1626
QY	1662	GATCAATATTTACAGTGGCTCTTCTGTATACTGTGTGGAGTACACTCTTATATAGAAAGTTCAA	1721
Db	1627	GATCAAAATTTTCGCGTCTCTCTGTATATAC -GTGGAGGTCACTCT - - -ATGAAGTCAA	1680
QY	1722	AAGCTATACGCTCTCTCTTTCTTCTTAACCTCAGTGAAGTAAATGGGGTCCGCTCAAGTTGA	1781
Db	1681	AAGCTATACGCTCTCTCTTTCTTCTTAACCTCAGTGAAGTAAATGGGGTCTGCTCAGATTGA	1740
QY	1782	AAGAGTCCATTTTTCACACTGTAGGCTGCGGTCGTGTGAATTTGAGCAGTCATTTTAACTGG	1841
Db	1741	AAGAGTCCATTTTTCACACTGTAGGCTGCGGTCGTGTGAATTTGAGCAGTCATTTTAACTGG	1800
QY	1842	CTTACAGGCTCTCCACACTTCTTTACGACCACTCTCTTTTTCAGTTGGCTGACTTCACACCC	1901
Db	1801	CTTCA - GCTTCCACACTCTTCTTACGACCACTCTCTTTTTCAGTTGGCTGACTTCACACCC	1859
QY	1902	TAGACATCATGAGTGGCAAGCAAAAAGAGAGAGACAATATACCGCGCGGGTTTTT	1961
Db	1860	TAGACATCATGAGTGGCAAGCAAAAAGAGAGAGACAATATACCGCGCGGTGTTTTT	1919
QY	1962	AGTTTGGGGGTTTGGCTTTCCCTTTTATGAGACCCATTCCTTATTAAGTCAATGT	2021
Db	1920	AGTTTGGGGGTTTGGCTTTCCCTTTTATGAGACCCATTCCTTATTAAGTCAATGT	1979
QY	2022	TTCTTTTATCACGATATTATTAGTAAGAAAACATCACTGAAATGCTAGCTGCAGTACA	2081
Db	1980	TTCTTTTATCACGATATTATTAGTAAGAAAACATCACTGAAATGCTAGCTGCAGTACA	2039
QY	2082	TTCTTTTGATGTCTAATGAGAAAGTTAAAAAGGTGGAATAATTCCTTGATTTCACAATGA	2141
Db	2040	TTCTTTTGATGTCTAATGAGAAAGTTAAAAAGGTGGAATAATTCCTTGATTTCACAATGA	2099
QY	2142	AATGCTCTCTTTTCCCTGCCCCAGAACCTTTTATCCACTTACCTAGATTCTACATATTC	2201
Db	2100	AATGCTCTCTTTTCCCTGCCCCAGAACCTTTTATCCACTTACCTAGATTCTACATATTC	2159
QY	2202	TTTAAATTTATCTGACAGGCTCCCTCAACCCAC	2235
Db	2160	TTTAAATTTATCTGACAGGCTCCCTCAACCCAC	2193

RESULT 4
 US-08-340-539A-1
 : Sequence 1, Application US/08340539A
 : Patent No. 5808025
 : GENERAL INFORMATION:
 : APPLICANT: Tedder, Thomas F.
 : APPLICANT: Kansas, Geoffrey S.
 : TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS

TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,539A
FILING DATE: 16-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gunnison, Jane
REGISTRATION NUMBER: 38,479
REFERENCE/DOCKET NUMBER: CG-104 CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 53..1207
US-08-340-539A-1

Query Match 92.4%; Score 2087.6; DB 1; Length 2330;
Best Local Similarity 98.5%; Pzed. No. 0;
Matches 2161; Conservative 0; Mismatches 24; Indels 9; Gaps 5;

QY 44 CCCTTGGCAAGGACCTGAGACCCCTTGTGCTAGTCAAGAGGCTCAATGSGCTGCAGAG 103
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DB 7 CCTTGGGCAAGGACCTGAGACCCCTTGTGCTAGTCAAGAGGCTCAATGSGCTGCAGAG 66
|||
QY 104 AACTAGAGAAGGACCAAGCAAGCCATGATATTTCATGGAATGTCAAGAGCACCAGAG 163
|||
DB 67 AACTAGAGAAGGACCAAGCAAGCCATGATATTTCATGGAATGTCAAGAGCACCAGAG 126
|||
QY 164 GCATTATGGAACATCTCAAGTTGTGGGGGGGAGCAATGCTCTGTGATTTCTGTCGC 223
|||
DB 127 GGCTTATGGAACATCTCAAGTTGTGGGGGGGAGCAATGCTCTGTGATTTCTGTCGC 186
|||
QY 224 ACATCATGGAACCTACTGCTGACATTCATTCATTTGAAAAACCATCAATGCGCAAG 283
|||
DB 187 ACATCATGGAACGACGATCTGTGACCTTACATTAATCTGAAAAACCATCAATGCGCAAG 246
|||
QY 284 GGCTAGAATATCTGCGGAGACAATTACAGATTTAGTTGCCATPACAAAGGCGGA 343
|||
DB 247 GGCTAGAATATCTGCGGAGACAATTACAGATTTAGTTGCCATPACAAAGGCGGA 306
|||
QY 344 AATTGATATCTGGAAGAAGCTCTGCGCTTCACTGTTCTTCACTGATGGAATCGG 403
|||
DB 307 AATTGATATCTGGAAGAAGCTCTGCGCTTCACTGTTCTTCACTGATGGAATCGG 366
|||
QY 404 GAAGATAGAGGAATATGAGCGTGGGTGGGAACAACAATCTCTCACTGAAGAAGCAGA 463
|||
DB 367 GAAGATAGAGGAATATGAGCGTGGGTGGGAACAACAATCTCTCACTGAAGAAGCAGA 426
|||

QY 464 GAAGTGGGAGATGTGAGCCCAACACAGAGAACAGAGAGACTGCTGAGATCTA 523
|||
DB 427 GAAGTGGGAGATGTGAGCCCAACACAGAGAACAGAGAGACTGCTGAGATCTA 486
|||
QY 524 TATCAAGAGAAACAAGATGCAGGCAAAATGAGACGACCTGCGACAACTAAAGGC 583
|||
DB 487 TATCAAGAGAAACAAGATGCAGGCAAAATGAGACGACCTGCGACAACTAAAGGC 546
|||
QY 584 AGCCCTGTGTACACAGCTTCTTGCCAGCCCTGCTCATGCAAGTGGCAATGTGT 643
|||
DB 547 AGCCCTGTGTACACAGCTTCTTGCCAGCCCTGCTCATGCAAGTGGCAATGTGT 606
|||
QY 644 AGAATCATCAATATACACACCTGCACTGTATGTTGGGGTCTATAGGCCCACTGTCA 703
|||
DB 607 AGAATCATCAATATATACACCTGCACTGTATGTTGGGGTCTATAGGCCCACTGTCA 666
|||
QY 704 GCTTGTATTCAGTGTGAGCCTTTGGAGGCCCCAGAGCTGGTACCATGAGACTGTCTCA 763
|||
DB 667 GTTGTATTCAGTGTGAGCCTTTGGAGGCCCCAGAGCTGGTACCATGAGACTGTCTCA 726
|||
QY 764 CCCCTTGGAACTTACGCTTACGCTCACAGTGTGCTTACGCTCTGGAAGAACAA 823
|||
DB 727 CCCCTTGGAACTTACGCTTACGCTCACAGTGTGCTTACGCTCTGGAAGAACAA 786
|||
QY 824 CTAACTGGGATTTGAAGAAACACCTGTGACCATTTTGGAACTGTATCTCCAGAAC 883
|||
DB 787 CTAACTGGGATTTGAAGAAACACCTGTGACCATTTTGGAACTGTATCTCCAGAAC 846
|||
QY 884 AACCTGTCAAGTATTCAGTGTGAGCCTCTATCAGCACCAGATTTGGGGATCATGAATCG 943
|||
DB 847 AACCTGTCAAGTATTCAGTGTGAGCCTCTATCAGCACCAGATTTGGGGATCATGAATCG 906
|||
QY 944 TAGCCATCCCTGCGCAGCTTACGCTTACCTGTGCAATGACCTTCACTCTCAGAAAG 1003
|||
DB 907 TAGCCATCCCTGCGCAGCTTACGCTTACCTGTGCAATGACCTTCACTCTCAGAAAG 966
|||
QY 1004 AACTGAGTTAATTTGGGAAGAAACCATTTGTAATCATCTGGAATCTGCTCAATACC 1063
|||
DB 967 AACTGAGTTAATTTGGGAAGAAACCATTTGTAATCATCTGGAATCTGCTCAATACC 1026
|||
QY 1064 TAGTCCATATGTCAAAAAATTTGGACAAAAGTTCTCAATGATTAAGAGGATTTATAA 1123
|||
DB 1027 TAGTCCATATGTCAAAAAATTTGGACAAAAGTTCTCAATGATTAAGAGGATTTATAA 1086
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QY 1124 CCCCTCTTCAATTCAGAGGAGCATGCTTACGCAATCTCTGCTGGATTTATCAT 1183
|||
DB 1087 CCCCTCTTCAATTCAGAGGAGCATGCTTACGCAATCTCTGCTGGATTTATCAT 1146
|||
QY 1184 TTGCTGGCAAGGAGATTAAGAAAGCAAGAAATCCACAGAGATTAAGATGCCATA 1243
|||
DB 1147 TTGCTGGCAAGGAGATTAAGAAAGCAAGAAATCCACAGAGATTAAGATGCCATA 1206
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QY 1244 TTTAATGCCCTTGTGTAAGAAAAATTTGGAATTAATAATCATGAGATCTTTAAA 1303
|||
DB 1207 TTTAATGCCCTTGTGTAAGAAAAATTTGGAATTAATAATCATGAGATCTTTAAA 1266
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QY 1304 TCTTCCATGAAGAGTTTGTGTGTGGGCACTCTACGTCACAAACATGAGATGTG -TTCC 1362
|||
DB 1267 TCTTCCATGAAGAGTTTGTGTGTGGGCACTCTACGTCACAAACATGAGATGTG -TTCC 1326
|||
QY 1363 TTCAAGTGCATGTGGGAAGATTTCTACCCGACCAAGATTCCTTACAGCTCAATTTGGCC 1422
|||
DB 1327 TTCAAGTGCATGTGGGAAGATTTCTACCCGACCAAGATTCCTTACAGCTCAATTTGGCC 1386
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QY 1423 CTCAATTAATCCCTTAACCCCGACCCAGCTGTTATACAGCTCAAGCTTTTGTCTTTT 1482
|||
DB 1387 CTCAATTAATCCCTTAACCCCGACCCAGCTGTTATACAGCTCAAGCTTTTGTCTTTT 1446
|||
QY 1483 CTGAGGAGAAACAATAAGACCAT -AAGGGAAGAGTTCAATGGAATTAAGAGGCT 1541
|||
DB 1447 CTGAGGAGAAACAATAAGACCATTAAGGGAAGAGATTCATGTTGGGAATTAAGAGGCT 1506
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QY 1542 GACTTGTCTCTTCTTGAATCTGTTTTCAGTTTCAATTCAGTGTGATGATGACAG 1601
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QY	1722	AAGCTACAGCTCTCCCTTCTTCTTAACACAGTGAAGTAATGGGGTCCGCTCAAGTTGA	1781
Db	1681	AAGCTACAGCTCTCCCTTCTTCTTAACACAGTGAAGTAATGGGGTCCGCTCAAGTTGA	1740
QY	1782	AAGAGTCTATTATTGGCACTGTAGCCCTGCGCTGTGTAATTGGACATTCCTATTTAACGTG	1841
Db	1741	AAGAGTCTATTATTGGCACTGTAGCCCTGCGCTGTGTAATTGGACATTCCTATTTAACGTG	1800
QY	1842	CTTCAGGCGCCGCCACCTCTTCTTCAAGCCACCTCTTCTTCAAGTGGCTACTTCCACAC	1901
Db	1801	CTTCA-GCCCTCCCACTCTTCTTCAAGCCACCTCTTCTTCAAGTGGCTACTTCCACAC	1859
QY	1902	TAGCATCTCATGAGTGCACCAAGCAAAAGAGAGAGAGAAATAGCCTCGGGTTTTTT	1961
Db	1860	TAGCATCTCATGAGTGCACCAAGCAAAAGAGAGAGAGAAATAGCCTCGGGTTTTTT	1919
QY	1962	AGTTTGGGGGTTTCTCTTCTTCTTATGAGACCACTTCTATTTTCTTATAGTCAATGT	2021
Db	1920	AGTTTGGGGGTTTCTCTTCTTCTTATGAGACCACTTCTATTTTCTTATAGTCAATGT	1979
QY	2022	TCTTTTATCAGATATTATTAGTAAGAAAACATCACTGTAATAGCTGAGTGCAGTGA	2081
Db	1980	TCTTTTATCAGATATTATTAGTAAGAAAACATCACTGTAATAGCTGAGTGCAGTGA	2039
QY	2082	TCTCTTTGATGTCATATGGAAGATTAANACGCTGAGAAATTCCTTGATTCACATGA	2141
Db	2040	TCTCTTTGATGTCATATGGAAGATTAANACGCTGAGAAATTCCTTGATTCACATGA	2099
QY	2142	AATGCTCTCTTCCCTCCGCCCCAGAACTTTATCCACTTACCTAGATTTACATATTC	2201
Db	2100	AATGCTCTCTTCCCTCCGCCCCAGAACTTTATCCACTTACCTAGATTTACATATTC	2159
QY	2202	TTTAAATTTCAATCTCAGGCTCCCTCAACCCAC	2235
Db	2160	TTTAAATTTCAATCTCAGGCTCCCTCAACCCAC	2193
RESULT 6			
5514582-1			
Patent No. 5514582			
APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.			
TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID			
IMMUNOGLOBULINS			
NUMBER OF SEQUENCES: 43			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/185,670			
FILING DATE: 21-JAN-1994			
Prior APPLICATION DATA:			
APPLICATION NUMBER: 986,931			
FILING DATE: 08-DEC-1992			
APPLICATION NUMBER: 808,122			
FILING DATE: 16-DEC-1991			
APPLICATION NUMBER: 440,625			
FILING DATE: 22-NOV-1989			
APPLICATION NUMBER: 315,015			
FILING DATE: 23-FEB-1989			
SEQ ID NO:1:			
LENGTH: 1829			
5514582-1			
Query Match 65.0%; Score 1469.2; DB 6; Length 1829;			
Best Local Similarity 90.3%; Pred. No. 0;			
Matches 1667; Conservative 0; Mismatches 3; Indels 176; Gaps 2;			
QY	1	GAATTCAGTGTCTGGTTCCTCCACCTGCAAGACAGACACATCCCTTTGGCAAGAGCCT	60
Db	1	gaatccagtgctgcttctcctcaaccgcgcaagaacacctcccttggcaaggacct	60
QY	61	GAGACCCCTTGCTAAGTCAAGAGGCTCAATGGCTGCGAGAACTAGAGAAGACCAA	120
Db	61	gagacccttgctgcttcaagagagctcaatggctgctgagaaactagagaagaccgaa	120

QY 121 GCAAGCATGATATTTCATGGAATGTCAGACACCGAGGAGCTTATGGAACATCT 180
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 Db 121 gcaagcatgatatttcataatgtaaatgtaagacacccagaggaactcttgaaactc 180
 QY 181 TCAAGTTGGGGGGTGGACAATGCTGTTGTTGATTTCTGGACATCATGGAACCTACT 240
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 Db 181 tcaagtggggggggtggaacaatgctctgtgtgtatctccggacacatcagaaactact 240
 QY 241 GCTGAGCTTACCATTTATCTGAAAAACCCATGAATCGCAAGGGCTTGAAGATTCTGCC 300
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 Db 241 gctgagcttaccattcttcgaaaaacccatgaaactggaaggctcagaagaattctggcc 300
 QY 301 GAGACATTTACAGATTTGTTGCCATTACAAAACAAGGGGAATTTGATTTCTGGAGA 360
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 Db 301 gagacattacacagatcttgccatacaaaaacagagcggaattgaaatcagaga 360
 QY 361 AGACTGCCCCCTTCAGTCTGTTTACTACTGATAGGAATCCGGAAGATAGGAATAT 420
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 Db 361 agactgcccccttcagtcgtcttactactgtaagaatccggaagatagaggaaat 420
 QY 421 GGAAGTGGGTGGGACCAACAAATCTCTCACTGAAGACAGAGAACTGGGAGATGTG 480
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 Db 421 ggaagtgggtgggacacaaatctctcactgaagaagagaaactggggagatgtg 480
 QY 481 AGCCCAACAAGAAAGAACAGAGAGAGTGGGATCTATATCAAGAAACAAG 540
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 Db 481 agcccaacaagaagaagaagagagacgctggagacatacaagaagaagaag 540
 QY 541 ATGCAAGCAAAATGGAAGATGACGCTGCCAACAATTAAGGACGCTTGTATTCACAG 600
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 Db 541 atgcaagcaaaatggaaagatgagacgctgccacaacaaagagagcccttgttacaag 600
 QY 601 CTTCCTGCAAGCCCTGGTCTATGCAATGGCCATGAGAAATGTGAAATCATATATC 660
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 Db 601 ctctctgcaagccctggctatgcaatggccatgagaatgtgaaatcatatc 660
 QY 661 AGACCTGCAAGCTGATGTTGGGTGATGAGGGCCAGTCTGATTCAGTGTGATTCAGTGTG 720
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 Db 661 agacctgcaagctgatggtggtggtatgagggccagttcagctgtgattcaggtg 720
 QY 721 AGCCTTGGAGGCCCGAGAGCTGGTACATGAGACTGTACTCAACCCCTTGGAACTTCA 780
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 Db 721 agccttggagggcccgagagctgtgacacatgaaactcacccttggaaactca 780
 QY 781 GCTTCAGCTCACAGTGTGCTTACGCTCTCTGAGGAACAATTAACCTGGATTCAG 840
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 Db 781 gcttcagctcacagtgcttccctcagctgtcctgaagaacaacttaactggatltgaag 840
 QY 841 AAACCACTGTGACATTTGGAACTGGTCAATCTCCAGAACCAACCTGTCAAGTATTC 900
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 Db 841 aaaccactgtgacatlttgaaactggtaactcctccagaaaccaactct----- 890
 QY 901 AGGTGAGCCTTATGACGACGATTTGGGATGATGAATCTGAGCACTGCCCTGGGCA 960
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 Db 901 aggtgagccttatacagcagatlttggggtatcagaaactgtagcaaccccttgagca 960
 QY 961 GCTTCAGCTTACCTCTGATGATGATCTTCACTGCTGAGGAAGAACTGATTAATGGA 1020
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 Db 961 gcttcagcttacctctgtcgtacacttcaactcctcaggaagaactgtaatttggga 1020
 QY 1021 AGAAGAAACCATTTTGTGAATCATCTGGAATCTGCTCAAACTCTAGTCCAAATGTCAAA 1080
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 Db 1021 agaagaacaacatttgaatcatctggaatctggtcaaaactcctagtcacaatltgcaaa 1080
 QY 1081 AATTTGCAAAAATTTCTCAATGATTAAGAGGGGTGATTTAAACCCCTTGTATTCACAG 1140
 |||||
 Db 1081 aatttgcaaaaatcttctcaatgataaggaagggtgattataaacccttcaatccag 1140
 QY 1141 TGGCACTCATGTTACTGATTCCTGCGGTGGCATTTATCATTTGGCTTGGCAAGAGAT 1200
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 Db 1141 tggcactcatgttactgattctctcgtgtggcttattatcatttgcgtgcaagagat 1200
 QY 1201 TAAAAAAGCAAGAAATCCAGAGAGATGATGATGACCATATTAATGCGCCCTTGCTG 1260

Db 1191 taataaaggcaagaatccaaaggaagtatgaatgacccatataatcgcccttggtg 1250
 QY 1261 AAGAAAAATTTCTTGGAAATTAATAATCATGAGATCCTTTAAATCTTCCATGAACGTT 1320
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 Db 1251 aaagaaatctcttgaaactaa----- 1274
 QY 1321 TTGTGTGTGGCACCTCTACGTCAACATGAACTGTGTTCTTCACTGCATCTGGGAAG 1380
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 Db 1275 ----- 1274
 QY 1381 ATTTCTACCCGACCAAGATTCTTCACTTCCATTTCCGCCCTCATTTATTCCTCAAC 1440
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 Db 1275 ----- 1274
 QY 1441 CCGACCCACAGTGTATTAACAGCTCAGCTTTTGTCTTTCTGAGAGAAACAATAA 1500
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 Db 1275 -----agtggtatacagctcagcttcttctccttctgagaggaacaaataa 1324
 QY 1501 GACCATTAAGGAAAGATTTATGATGGAATTAAGATGGCTGACTTGTCTTTCTTGAC 1560
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 Db 1325 gaccataaggaaagatcatatgtgaaataaaagatgctgacatctgtccttctgac 1384
 QY 1561 TCTTGTTCAGTTCAATTCACTGCTGTACTTGTATGACAGACACTCTAAATGAAGTGC 1620
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 Db 1385 tcttglttcaaglttcaatcactcagctgtccttctgacatgacacactctaaatgaagtc 1444
 QY 1621 AAATTTGATACATATGTAATATGAGACTCAGTTTCTTGGAGATCAAAATTCACGTGTC 1680
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 Db 1445 aaattgatacatatgtgaatagactcagtttcttctgagatcaaatltcaagtcg 1504
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 Db 1505 ttcgtatactgtgaggtacactctataagaaagttcaaaagttcacgctccttctc 1564
 QY 1741 TTTCTACTCAGAGATGATGAGGTCCTGCTCAACTTGAAGAGCTCATTTTGGCACTG 1800
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 Db 1565 tttcctaacctccaggaagatagtggtccgtcccaagttgaagaagttccatltgacgt 1624
 QY 1801 TAGCCTGCGCGTGTGTAATTTGGACATTCCTATTAACTGGCTTCA 1846
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 Db 1625 tagcctgcgctgtgtaattggaacatcctatttaacttgcttca 1670

RESULT 7
 US-08-340-539A-11
 ; Sequence 11, Application us/08340539A
 ; Patent No. 5808025
 ; GENERAL INFORMATION:
 ; APPLICANT: Tedder, Thomas F.
 ; APPLICANT: Kansas, Geoffrey S.
 ; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
 ; TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FISH & NEAVE
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10020
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/340,539A
 ; FILING DATE: 16-NOV-1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/008,459
 ; FILING DATE: 25-JAN-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Gunnison, Jane
 REGISTRATION NUMBER: 38,479
 REFERENCE/DOCKET NUMBER: CG-104 CON
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-596-9000
 TELEFAX: 212-596-9090
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1696 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-340-539A-11

Query Match 40.8%; Score 922.2; DB 1; Length 1696;
 Best Local Similarity 97.8%; Pred. No. 3.2e-261;
 Matches 989; Conservative 0; Mismatches 13; Indels 9; Gaps 5;

1227 AGTATGATGACCATATTAATGCGCCCTGGTGAAGAAATTTCTGGAACTATAAAA 1286
 308 AGTATGATGACCATATTAATGCGCCCTGGTGAAGAAATTTCTGGAACTATAAAA 367
 1287 TCATGATGATGATTAATGCGCCCTGGTGAAGAAATTTCTGGAACTATAAAA 1346
 368 TCATGATGATGATTAATGCGCCCTGGTGAAGAAATTTCTGGAACTATAAAA 427
 1347 ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1405
 428 ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 487
 1406 CAGCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1465
 488 CAGCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 547
 1466 TCAGCTTTTGTCTTTTGTGAGAGAAATTAAGACATTAAGGAAAGATTCATGT 1524
 548 TCAGCTTTTGTCTTTTGTGAGAGAAATTAAGACATTAAGGAAAGATTCATGT 607
 1525 GGAATATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1584
 608 GGAATATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667
 1585 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1644
 668 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 727
 1645 GACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1704
 728 GACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 786
 1705 CTATATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1764
 787 CTATATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 841
 1765 GCTGCTGCTCAAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1824
 842 GCTGCTGCTCAAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 901
 1825 CCATGCTATTAAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1884
 902 CCATGCTATTAAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 960
 1885 TGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1944
 961 TGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 1945 AGCTGCGCGGTTTTTATGTTGGGGTTTTTGTGTTTCTTTTATGAGACCATTCCTA 2004
 1021 AGCTGCGCGGTTTTTATGTTGGGGTTTTTGTGTTTCTTTTATGAGACCATTCCTA 1080

2005 TTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2064
 1081 TTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 2065 GCTAGCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2124
 1141 GCTAGCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 2125 TCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2184
 1201 TCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 2185 CTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2235
 1261 CTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1311

RESULT 8

US-08-461-592B-11
 Sequence 11, Application US/08461592B

GENERAL INFORMATION:
 PATENT NO. 5834425
 APPLICANT: Tedder, Thomas F.
 TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
 TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESS: Weingarten, Schurgin, Gagnebin & Hayes
 STREET: Ten Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/461,592B
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/340,539
 FILING DATE: 16-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/008,459
 FILING DATE: 25-JAN-1993

ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: CG-104
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 TELEX: 14-8367
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1696 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-461-592B-11

Query Match 40.8%; Score 922.2; DB 2; Length 1696;
 Best Local Similarity 97.8%; Pred. No. 3.2e-261;
 Matches 989; Conservative 0; Mismatches 13; Indels 9; Gaps 5;

QY 1227 AGATGATGACCATATTAATGCGCTTGGTGAAGAAAATTTCTGAATACTAAAA 1286
 Db 308 AGATGATGACCATATTAATGCGCTTGGTGAAGAAAATTTCTGAATACTAAAA 367
 QY 1287 TCATGAGATCCTTTAAATCCTTCATGAAACGTTTTGTGTGGACCTCTACGTCA 1346
 Db 368 TCATGAGATCCTTTAAATCCTTCATGAAACGTTTTGTGTGGACCTCTACGTCA 427
 QY 1347 ACATGAAGTGTG-TTCCCTCAGTGCATCTGGGAAGATTCTACCCAGCAACGTTCTT 1405
 Db 428 ACATGAAGTGTGTTCTTTCAGTGCATCTGGGAAGATTCTACCCAGCAACGTTCTT 487
 QY 1406 CAGCTTCCATTTGCGCCCTCATTTATCCCTCAACCCCGACAGGTGTTATACAG 1465
 Db 488 CAGCTTCCATTTGCGCCCTCATTTATCCCTCAACCCCGACAGGTGTTATACAG 547
 QY 1466 TCAGCTTTTGTCTTTCTGAGAGAGAAACAATTAAGACCAT-AAAGGAAAGATTCATGT 1524
 Db 548 TCAGCTTTTGTCTTTCTGAGAGAGAAACAATTAAGACCATAAAGGAAAGATTCATGT 607
 QY 1525 GGAATATTAAGATGGCTGACTTGTCTTTCTGACTCTGTTGTTCAAGTTCAATTCACT 1584
 Db 608 GGAATATTAAGATGGCTGACTTGTCTTTCTGACTCTGTTGTTCAAGTTCAATTCACT 667
 QY 1585 GGTGACTGATGACAGACACTTCTAAATGAAGTGAATTTGATACATATGTGAATATG 1644
 Db 668 GGTGACTGATGACAGACACTTCTAAATGAAGTGAATTTGATACATATGTGAATATG 727
 QY 1645 GACTCAGTTTTCCTGAGATCAAAATTTACAGTCTCTTCTGATACGTGAGAGTCACT 1704
 Db 728 GACTCAGTTTTCCTGAGATCAAAATTTCCGCTGCTCTCTGATAC-GTGGAGGTCACT 786
 QY 1705 GTTATAGAAAGTTCAAAAAGCTACGCTCTCTTCTTCTAACTCAGTGAAGTATGG 1764
 Db 787 CT-----ATGAAGTCAAAAGCTACGCTCTCTTCTTCTAACTCAGTGAAGTATGG 841
 QY 1765 GGTCCGCTCAAGTGAAGAGTCTATTTGACATGACCTGCGCTGTGTAATTTGA 1824
 Db 842 GGTCCGCTCAAGTGAAGAGTCTATTTGACATGACCTGCGCTGTGTAATTTGA 901
 QY 1825 CCATCTATTTAACTGGCTTCCAGCCCTCCCACTCTTTCAGCCACCTCTCTTTTCACT 1884
 Db 902 CCATCTATTTAACTGGCTTCCAGCCCTCCCACTCTTTCAGCCACCTCTCTTTTCACT 960
 QY 1885 TGGCTGACTTCCACACCTTGCATCTCATGATGATGCCAAGCAAAAGAGAGAGAAAT 1944
 Db 961 TGGCTGACTTCCACACCTTGCATCTCATGATGATGCCAAGCAAAAGAGAGAGAAAT 1020
 QY 1945 ACCCTGCGGGTTTTTATTTGGGGGTTTTGCTGTTCTTTATGAGACCATTCCTA 2004
 Db 1021 ACCCTGCGGGTTTTTATTTGGGGGTTTTGCTGTTCTTTATGAGACCATTCCTA 1080
 QY 2005 TTTCTTATAGTCAATGTTCTTTTATCAGATATTTATGTAAGAAACATCACTGAAT 2064
 Db 1081 TTTCTTATAGTCAATGTTCTTTTATCAGATATTTATGTAAGAAACATCACTGAAT 1140
 QY 2065 GCTAGCTGACATGATCTTTGATGTCATATGGAAGATTAAAAAGAGTGGAGAAAT 2124
 Db 1141 GCTAGCTGACATGATCTTTGATGTCATATGGAAGATTAAAAAGAGTGGAGAAAT 1200
 QY 2125 TCCCTGATTCACAATGAAATGCTTCCTTCCCTGCGCCCGCAAGACTTTTATCCACTTAC 2184
 Db 1201 TCCCTGATTCACAATGAAATGCTTCCTTCCCTGCGCCCGCAAGACTTTTATCCACTTAC 1260
 QY 2185 CTAGATTTCTACATATTTCTTTAAATTTCAATGAGGCTCCCTCAACCCAC 2235
 Db 1261 CTAGATTTCTACATATTTCTTTAAATTTCAATGAGGCTCCCTCAACCCAC 1311

RESULT 9
 US-08-513-278-3
 ; Sequence 3, Application US/08513278
 ; Patent No. 5840844

; GENERAL INFORMATION:
 ; APPLICANT: LASKY, LAURENCE A.
 ; APPLICANT: STACHELL, SCOTT E.
 ; APPLICANT: ROSEN, STEVEN D.
 ; APPLICANT: SINGER, MARK S.
 ; APPLICANT: YEDNOCK, TED A.
 ; TITLE OF INVENTION: LYMPHOCTE HOMING RECEPTORS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/513,278
 ; FILING DATE: 10-AUG-1995
 ; CLASSIFICATION: 5530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/059027
 ; FILING DATE: 06-MAY-1993
 ; APPLICATION NUMBER: 07/786149
 ; FILING DATE: 31-OCT-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/315015
 ; FILING DATE: 23-FEB-1989
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Ginger R.
 ; REGISTRATION NUMBER: 33,055
 ; REFERENCE/DOCKET NUMBER: 565D1C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-3216
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2214 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-513-278-3

Query Match 37.9%; Score 856.8; DB 2; Length 2214;
 Best Local Similarity 73.4%; Pred. No. 6,2e-242;
 Matches 1160; Conservative 0; Mismatches 392; Indels 28; Gaps 4;

QY 92 GGGCTGAGAGAACTAGACAGACCAAGCAGCATGATATTTCCATGGAATGTCA 151
 Db 69 GGGCTGAGAGAACTAGACAGACCAAGCAGCATGATGTTTCCATGAGATGTGA 128
 QY 152 GAGCACCAGAGAGGACTTATGGAACATCTTCAAGTTGTGGGGTGGACAATGCTGTG 211
 Db 129 GGGTACTTACTGGGGCTCGAGAAACATCTGAAAGTGTGGGTGCGACACTGCTGTG 188
 QY 212 TGATTTCTGGGACATCATGAGAACCTACTGCTGAGACTTACCATTTATCTAAAAACCAT 271
 Db 189 TGACTTCTGGATACACCATGGAACCTACTGTTGACTTACCATTTATCTAAAAAGCCAT 248
 QY 272 GAACGTGCAAGGGCTAGAAAGATTCTGCCGAGACAATTACAGATTATAGTGCATACA 331
 Db 249 GAACGTGCAAGGGCTAGAAAGATTCTGCCGAGACAATTACAGATTATAGTGCATACA 308
 QY 332 AAACAAGGGCGAAATGAGATATCTGGAGAGAGACTGCGCTTCACTGCTTACTACTG 391
 Db 309 AAACAAGAGAGAAATGAGATATTTAGAGATATCATTTGCCCAAAAGCCCTTATTACTACTG 368

OY	392	GATGGAAATCCGGAAATPAGAGAAATPAGACGTCGGGTGGGAAACCAACAATCTCTAC	4451
Db	369	GATGGAAATCAGGAAAAATTGGAAAAATGGACATGGGGTGGGAAACCAACAATCTCTAC	4428
OY	452	TGAAGAACGAGAACTGGGGAGATGGTAGGCCCAACAAGAGAAACAAGAGAGACTG	5111
Db	429	TAAAGAGCAGAGAACTGGGGGTCTGGGGAGGCCAACAAGAAAGTCCAAAGAGACTG	4488
OY	512	CGTGGAAATCTATATCAAGGAAACAABAATCGAGCAATGGAAAGATGAGCGCTGCCA	5711
Db	489	TGTGGAAATCTATATCAAGGAGGAAACGAAACACTCTGGGAAATGGAAACGATGAGCGCTGCA	5448
OY	572	CAAACTAAAGCGACCCCTGTGTACACAGCTCTTGCCAGCCCGTGCATCACTAGTGGCCA	6311
Db	549	CAAAACGAAAGGAGCTCTCTGCTGACACAGCCCTTGCCAGCCAGGCTTGTGCAATGGCCG	608
OY	632	TGGAGATGTGTGAATATATCAATATACACCTGCACCTGATGTGGGTACTATGG	6911
Db	609	TGGAGATGTGTGGAATATCAATCAACACCTGCATCTGTATCAGAGGTATTCAGG	668
OY	692	GCCCCAGTGTACAGCTGTATTCAGTGTGAGCGCTTGGAGGCCCAAGCGGGTACAT	7511
Db	669	GCCCCAGTGTACAGTGTATGTGTCCATGTGAGCCTTTGGAGGCCCTTGAATTTGGTACAT	728
OY	752	GGAGCTACTCACCCCTTTGGAACTTAGCTTCACTCAGTCAGTGTGCTTCAGTCTC	8111
Db	729	GGAGCTCATTCACCCCTTGGGAACTTCAAGCTTCAGTCCAGTCCAAAGTGTCTTCAACTGTTC	788
OY	812	TGAAGCAAACTTAACGGGATGGAAGAAACCACTGGAGCAATTTGGAAACGTGTC	8711
Db	789	TGAGGAGAGAGAGTACTTGGGACGTGCAAGAACACACTGTGTGACATCTGGAACGTGTC	848
OY	872	ATCTCCAGAACCACTGTCAAGTGTACGTGTGAGCTCTATACAGCACGATTTGGG	9311
Db	849	ATCTCCAGAGCAACTGTCCAAAGTGTCTCAGTGTGAGCCTTTGGAAGCCCTGAGTTGGG	908
OY	932	GATCATGAATCTATACCAATCCCGGCGAGGTTCAGGTTTAACTGTGATTCCTTCAT	9911
Db	909	TACATGAGATCTGATCCACCCCTTGGAAACTTCAAGTTCACAGTGTGCTTCAA	968
OY	992	CTGTCTCAGAGAGACTGATTAATTTGGGAAAGAAACCATTGTGAATCAATCTGGAAAT	10511
Db	969	CTGTCTCAGAGAGAGAGAGTACTTGGGACTGCAGAAACACAGTGTGAGCANTCTGGAAA	10222
OY	1052	CTGGTCAATCTGATGTCACAAATATGTCAAAAATTGGACAAAAGTTTCTCAATATPAGA	111111
Db	1029	CTGGTCAATCTGACAGACCAATCTGCAAGAGACAAACAGAAAGTTTCTCAAAATCAAAGA	10888
OY	1112	GGGTGATTAACCCCTCTTCTCATTCAGTGGCAGATCATGTTAGCTCATCTCGGGAT	11711
Db	1089	AGGTGATTAACACCCCTCTTCTCATTCAGTGGCAGATCATGTTAGCTCATCTCGGGCT	11488
OY	1172	GGCATTTTCAATTTGGCTGGCGAAGAGATTTAAAAAAGCAAGAAATCCACAGAGATAT	12311
Db	1149	GGCATTTTCTCAATTTGGCTGGCGAAGGGGTTAAAAAAGCAAGAAATCTCAAGAAAGAT	1208
OY	1232	GAATGACCATAATTAATCCGCCCTTGATGGAAGAAATAATCTTG-----GAATCTTAA	1284
Db	1209	GGATGATCATACATGATTCATCTTTGTGAAAGGAAGCAATGAAGTCTATAGCAAAA	1268
OY	1285	AATCATGAGATCCCTTTAATCTCTTCATGAAAGCTTTGTGTGTGGCAGCTCTCTAGCTC	1344
Db	1269	CATTGAAAAATTAACGTCAACTCTCTCCGTGAAGATTTTACAGCGAGGATCTCCACATTT	1328
OY	1345	AAACATGAAGTGTGTCCTTCAGTGCATGGGAGATTTTACCCGCAACAGTTCCT	1404
Db	1329	AGAGATCATGATTTGCT--TCAACGAATCTGGAAGGATTTTCTCATGACGCAACAGCTCT	1386
OY	1405	TCACTTCATTTGGCCCTCATTTATCCCTCAACCCCAAGCCCAAGGTGTTATACG	1464
Db	1387	CTGTAATTTCCCTGCTGCTCATTCATCCATTAACCTATTCACATATGTTGTATACAG	1446
OY	1465	CTCAGCTTTTGTCTTTCTTGAGGAGAAACAATTAAGCACTTAAGGAAAGATTCATGT	1524

Accession	Sequence	Position
Db	1447 AGTAGTATTATTCATCTTTTCGTGTGAGAAC-----AAGCAAAAGCTTACTGT	1497
OY	1525 GGATATTAAGATGCGCTGACTTTGCTCTTTCTTGACTCTGTTTCAGTTCACTTAATTCAGT	1584
Db	1498 AGAATATTAAGACAGCGCGCTTTAGCTTCTTCACCTCTGTTTCCCTAGTCAATTCAGC	1557
OY	1585 GCTGTACTTGATGACACACACTCTTAATGAAGTGCATATTTGATCATATGTAATATG	1644
Db	1558 ACAGAACCTATATGCCAACAC-----AGTGAATATATGATCCATGAGTATTTGGA	1607
OY	1645 GATCTGACTTTTCTTGACGAT	1664
Db	1608 AACTCAGACTCTTTGGCCAT	1627

RESULT 10
 5514582-3
 Patent No. 5514582
 APPLICANT: CASRON, DANIEL J.; TASKY, LAURENCE A.
 TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
 IMMUNOGLOBULINS
 NUMBER OF SEQUENCES: 43
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/185,670
 FILING DATE: 21-JAN-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 986,931
 FILING DATE: 08-DEC-1992
 APPLICATION NUMBER: 808,122
 FILING DATE: 16-DEC-1991
 APPLICATION NUMBER: 440,625
 FILING DATE: 22-NOV-1989
 APPLICATION NUMBER: 315,015
 FILING DATE: 23-FEB-1989
 SEQ ID NO:3
 LENGTH: 2214
 5514582-3

Query Match	37.9%	Score 856.8	DB 6	Length 2214
Best Local Similarity	73.4%	Pred. No. 6.2e-242		
Matches 1100	Conservative	0	Mismatches 392	Indels 28
				Gaps 4
QY	92	GGGCTCAGAGAAGACTAGAGAAGGACCAAGCAAGCCATGATATTTCCATGGAAAATGTCA	151	
Db	69	ggcctcgagagagactcgtagagagagagcccaagaagcagatggtttccatctgtagatgta	128	
QY	152	GAGCACCAGAGGGACTTATGGAACATCTTCAAGTTGTGGGGGTGGACAAATCCTGTGG	211	
Db	129	gggtactactctggggtcggagaaacatcctggaagctgtggtgctgagacactctgtg	188	
QY	212	TGATTTCTCGGACATCATGGAACCGTACGCTGCGACTTACATTTATTCGAAAAACCAT	271	
Db	189	tgacttcctgatacaccatcagacacacacgtgttgacttaccatcttctgaaagccat	248	
QY	272	GAACTGGCAAAAGGCTAGAAAGTTTGGCCGAGACAATTCACAGTAATGTTGCCATACA	331	
Db	249	gaacttgggaaaaatgcttagaaagtcttgcgaagaagaataatcacaaagtttagtcgcataca	308	
QY	332	AAACAAAGCGGGAATTTAGTATCTCGAAGACGCTGGCCCTGAGTGGTTCCTACTAG	391	
Db	309	aaacaaagagagaatttgatgtattcttagaataacatctgccaaaagccctatctactg	368	
QY	392	GATAGGAATCCGGGAAGATAGAGAAATATGACGTGGGTGGGAACCAACAATCTCTCAC	451	
Db	369	gataggaatcagaaaaatcttgysaaaatcttgcacatggttggysaaaccaaaaactctcac	428	
QY	452	TGAACAACACAGGAAGCTGGGGGAAATGGTGAGCCCAACAACAAGAAACAAGAGGACTG	511	
Db	429	taagaagcagagaagacttgggtgctctggggagcccaacaacaagaagctcaagysagactg	488	
QY	512	CGTGAGATCTATATCAAGAGAAACAAGATGCGGCAAAATGGAACATATACGCTCCCA	571	

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Db 489 tggggagatcatatcatcaaggaggagacgagactctgggaatatggaacgatgaagcgtctca 548
      |||
QY 572 CAACCTAAAGGACCCCTGTTTACACAGCTTCTTGCCAGCCCTGGTCATGACAGTGGCCA 631
      |||
Db 549 caaagaaagagcgtctctgtctacacagcctctgtccagcaggtcttgcaatgagcg 608
      |||
QY 632 TGGAGAAATGCTGAGAAATCATCATATATCACACTGCACTGTATGTGGGTACTATGG 691
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Db 609 tggagaatggtggaacatcaacaacacgctgcatctgtatgacaggtatctacg 668
      |||
QY 692 GCCCCAGTGTGAGCTTGTGATTCAGTGTGAGCCCTTTGGAGCCCCCAAGCGGGGTACCAT 751
      |||
Db 669 gccccagtgctcatatgtgtgtccagtgtagccttggaagccccctgagtgtgtaccat 728
      |||
QY 752 GGAAGTACTACCCCTTTGGAAACTTCAGCTTCAGCTCAGTGTGCTTCAGCTGCTC 811
      |||
Db 729 ggaactgcaccaccttggaacttcagcttcacagtgcttcacactgttc 788
      |||
QY 812 TGAAGGAAACAACTTAACCTGGGATTTGAAGAACCCACTGTGGACATTTGGAACTGTC 871
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Db 789 tggaggaaagaaactacttggagctgcagaaacacagtgtagacatctgaaactgttc 848
      |||
QY 872 ATCTCCAGAACCAACCTGTCAGTGTGAGCTGTGAGCTCTATACAGCACAGATTTGGG 931
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Db 849 atctccagagccaaactgtccaaagtgtccagtgtagccttggaagccccctgagtggtg 908
      |||
QY 932 GATCATGAACTGATGACCATCCCTGGCCAGCTTCAGCTTACCTTCATGATACCTTCAT 991
      |||
Db 909 taccatgtagctacatccacccttggaacttcagcttcacagtgagtggttcacaa 968
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QY 992 CTGCTCAGAAGAACCTGATTAATTTGGGAAGAAACCAATTTGTATCATCTGCAAT 1051
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Db 969 ctgtctgaggagaaagagtagcttggagctgcagaaacacagtgtagacatctgga 1028
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QY 1052 CTGTGCAAACTAGTACCATATGTCAAAATTTGACAAAATTTTCATGATTAAGA 1111
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Db 1029 ctgtgtatctccagagcaactctgcagaaagacaaagaaagttctccaaagtcaaga 1088
      |||
QY 1112 GGGTATTAATACCCCTCTTCATTCAGTGCAGTGCATGATTCATCTCTGGGT 1171
      |||
Db 1089 aggtgactacaacccccctctctctctctgtagcgcgtatgltcacgcgcatctcgg 1148
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QY 1172 GGCATTTATCATTTGGCTGGCAGAGATTAATAAAGGCAAGAAATCCACAGAAATAT 1231
      |||
Db 1149 ggcattctcatctgtgctggaagcggttaaaaaaggaagaaatctcaagaagaagat 1208
      |||
QY 1232 GAATGACCCCATTTAAATCGCCCTGGTGAAGAAATTTCTTG-----GAATACTAAA 1284
      |||
Db 1209 ggaatgacatcatgactatcctctgtgaaagaaagcaatgaagtgtcaaaagacaaa 1268
      |||
QY 1285 AATCATGAGATCTTAAATCTTCATGAAAGCTTTGTGGTGGACACCTCTCTACGTC 1344
      |||
Db 1269 catgtgaaataatcgaagctctcccgtagaagatttacaacgagcgtctccacatc 1328
      |||
QY 1345 AACATGAAAGTGTGCTTCTTCACTGATCTGGGAAGATTTCTACCCGACCAAGTTCTT 1404
      |||
Db 1329 agagaaatgagctgttgc--tcaacgaatctggaagatcttcatatgcaaaagcctc 1386
      |||
QY 1405 TCAGCTTCATTTGCGCCCTCATTTATCCCTCAACCCCGCCACAGGTTTATTCAG 1464
      |||
Db 1387 cctaattcccccgcgtcatcatcatccatcaaccatcccaataatgtgtgtctatacag 1446
      |||
QY 1465 CTCAGCTTTTGTCTTTCTGTAGAGAAACAAATTAAGACCATTAAGGAAAGATTCATGT 1524
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Db 1447 agtagaattatcatcattcttcgtgagaac-----aagcaaaagtgtactgt 1497
      |||
QY 1525 GGAATTAAGATGCTGACTTTGCTTCTTGTGACTCTTGTGCTTGTGCTTCAATTCAGT 1584
      |||
Db 1498 agaataataagaaagcgtcttactcttctcctaaactgttctccagttcaatltcagc 1557
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QY 1585 GCCTGCTTGTATGACAGACACTTCTAAATGAAGTCAAATTTGATACATATGTGAATATG 1644
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Db 1558 acagaagctaatgccaacac-----agtgaatatatgtatccatgtgtaattgga 1607
QY 1645 GACTCAGTTTCTTGACAGAT 1664
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Db 1608 aactcagactctctgtcgcat 1627

RESULT 11
US-08-340-539A-5
; Sequence 5, Application US/08340539A
; Patent No. 5808025
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; APPLICANT: Kansas, Geoffrey S.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULANEUS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,539A
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,459
; FILING DATE: 25-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gunnison, Jane
; REGISTRATION NUMBER: 38,479
; REFERENCE/DOCKET NUMBER: CG-104 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-340-539A-5

Query Match 17.1%; Score 385.2; DB 1; Length 531;
Best Local Similarity 99.2%; Pred. No. 1.2e-103;
Matches 387; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 213 GATTTCCTGGACATCATGTGAACCTACTGTGGAATTAATTCGAAAAACCCATG 272
      |||
Db 72 GATTTCCTGGACATCATGTGAACGACGCTGGAATTAATTCGAAAAACCCATG 131
      |||
QY 273 AACTGGCAAAAGGCTAGAAATTTCTGCCGAGACAAATTACACAGATTTAGTTGCCATACAA 332
      |||
Db 132 AACGGGCAAAAGGCTAGAAATTTCTGCCGAGACAAATTACACAGATTTAGTTGCCATACAA 191
      |||
QY 333 AACAAAGCGGAAATTTGAGTATCTGAGAAAGACTGTGCCCTTCAGTGTCTTACTACTGG 392
      |||
Db 192 AACAAAGCGGAAATTTGAGTATCTGAGAAAGACTGTGCCCTTCAGTGTCTTACTACTGG 251
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QY 393 ATAGAAATCCGGAAGATAGAGAAATATGACGTGGGTGGGAACCAACAATCTCTCACT 452
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Db 252 ATAGAAATCCGGAAGATAGAGAAATATGACGTGGGTGGGAACCAACAATCTCTCACT 311
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QY 453 GAAGAACGAGAACTGGGGAGATGTGAGCCCAACAAGAAAGAACAGAGACTGC 512
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Db 312 GAAGAACGAGAACTGGGGAGATGTGAGCCCAACAAGAAAGAACAGAGACTGC 371
QY 513 GTGAGATCTATATCAAGAAACAAAGATGAGCAATGAGACGCTGCCAC 572
|||||
Db 372 GTGAGATCTATATCAAGAAACAAAGATGAGCAATGAGACGCTGCCAC 431
QY 573 AAACAAAGGACGCTCTGTACACAGCT 602
|||||
Db 432 AAACAAAGGACGCTCTGTACACAGCT 461

RESULT 12
US-08-461-592B-5
; Sequence 5, Application US/08461592B
; Patent No. 5834425
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; APPLICANT: Kansas, Geoffrey S.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
; TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurigin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,592B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/340,539
; FILING DATE: 16-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,459
; FILING DATE: 25-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: CG-104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: 14-8367
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-461-592B-5

Query Match 17.1% Score 385.2; DB 2; Length 531;
Best Local Similarity 99.2%; Pred No. 1.2e-103;
Matches 387; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 213 GATTTCTGGACATCAGGAACCTACTGACTTACCATTTATTTGAAAAACCATG 272
|||||
Db 72 GATTTCTGGACATCAGGAACCTACTGACTTACCATTTATTTGAAAAACCATG 131

QY 273 AACTGCAAAAGGCTTAGAGATTTCTGCCAGACAAATTACACAGATTAGTGGCATACAA 332
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Db 132 AACTGCAAAAGGCTTAGAGATTTCTGCCAGACAAATTACACAGATTAGTGGCATACAA 191
QY 333 AACAAAGCGGAAATTTGATCTGAGAGACTCTGCCCTTCAGTGCTTTACTACTG 392
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Db 192 AACAAAGCGGAAATTTGATCTGAGAGACTCTGCCCTTCAGTGCTTTACTACTG 251
QY 393 ATAGAAATCCGGAAGATAGAGAAATATGAGCTGGTGGGAACCAAAATCTCTACT 452
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Db 252 ATAGAAATCCGGAAGATAGAGAAATATGAGCTGGTGGGAACCAAAATCTCTACT 311
QY 453 GAAGAACGAGAACTGGGGAGATGTGAGCCCAACAAGAAAGAACAGAGACTGC 512
|||||
Db 312 GAAGAACGAGAACTGGGGAGATGTGAGCCCAACAAGAAAGAACAGAGACTGC 371
QY 513 GTGAGATCTATATCAAGAAACAAAGATGAGCAATGAGACGCTGCCAC 572
|||||
Db 372 GTGAGATCTATATCAAGAAACAAAGATGAGCAATGAGACGCTGCCAC 431
QY 573 AAACAAAGGACGCTCTGTACACAGCT 602
|||||
Db 432 AAACAAAGGACGCTCTGTACACAGCT 461

RESULT 13
US-08-365-470-2
; Sequence 2, Application US/08365470
; Patent No. 5632991
; GENERAL INFORMATION:
; APPLICANT: Gimbrone, Jr., Michael A.
; TITLE OF INVENTION: Antibodies Specific For E-selectin And The Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,470
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,510
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/850,802
; FILING DATE: 13-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Markowicz, Karen R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 0627.1350003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: nucleic acid
; LOCATION: 1-1833
; OTHER INFORMATION: / label - nucleic acid

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; OTHER INFORMATION: /note - SEQ ID NO:2 begins at base pair position 117 and ends
; OTHER INFORMATION: base pair position 1949.
US-08-365-470-2

Query Match      13.7%: Score 310; DB 1; Length 1833;
Best Local Similarity 60.6%: Pred. No. 2.9e-81;
Matches 508; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

QY 242 CTGGACTTACCATTTATCTGAAAAAACCATGAACCTGGCAAGGCTTGAAAGATTCGCCG 301
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DB 63 CTGGCTCTTACAAACACCTCCACGAGCTATGACTTATGATGAGGCCAGTCTTATCTGCA 122
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 302 AGCAATTCACAGATTTACTTCCATACAAAACAGCGGAAATTAGTATCTGGGAA 361
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 123 GCAAGGTACACACCTGGTTCATTTCAAAACAAAGAGATTCAGTACCTAAATCTC 182
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 362 GACTCTGCCCTTACGTCGTTCTTACTACTGATAGAAATCCGGAAGTATGAGAGATATG 421
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 183 CATATTGAGCTATTACCAAGTTTATTCTGATTGGATTGGAATGAAAAGTCAACATGTGTG 242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 422 GAGCTGGGTGGGAACCAAAATCTCTCACTGAAGAAGAGAACTGGGAGATGGTGA 481
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 243 GGTCTGGGTGGAACCCAGAAACCTCTGACAGAAGAACCAAGAACCTGGCTCCAGGTGA 302
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 482 GCCCAACACAAAGAACAGAGACACTCGTGGAGATTTATATCAAGAAACAAGA 541
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 303 ACCCAACAAATAGGCAAAAMATAGGACTCGTGGAGATTTACTATCAAGAGAAAAAGA 362
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 542 TGCAGGCAATAGGACGATAGCGCTGCCACAAACTAAAGCAGCCCTGTTACACAGC 601
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 363 TGTGGGCAATGGAATGATAGAGGTGCACAGAAAGAACTGGCTTATGCTACACAGC 422
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 602 TTCTTGCCACCCCTGTGTCATGAGTGGCCATGAGAAATGTGTAGAAATCATATAATCA 661
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 423 TGCCTGACCAATATACATCTGTCAGATGGCCACGGGAATGTGTAGAGCAATCATATAATTA 482
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 662 CACTCTGCACTGTGATGTGGGGTACTATGGGCCCACTGTGACCTTGTGATTCAGTGTGA 721
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 483 CACTTTCMACTGTGACCCCTGCTTCACTGACTCAACTGACCTCAAAATTTGTGAACCTGTAC 542
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 722 GCCTTTGAGAGCCCAAGAGTGGGTATACATGAGTACTACCCCTTGGAAACTTCAG 781
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 543 AGCCCTGGAATCCCTCTGAGATGAGAGTGGTTTGTGACAGTACCCACTGGGAAACTTCAG 602
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 782 CTTCACCTCAGACTGTGCTTCTGAGCTGCTTGAAGAAACAACCTTAACTGGATGAGA 841
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 603 CTACAAATTTCTTCTGCTATACAGCTGTGATAGGGGTTTACTGCAAGCAGCATGGAGAC 662
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 842 AACCACTGTGGACATTTTGGAAACTGTATCTCCAGAAACAACCTGTCAAGTGAATCA 901
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 663 CAGTCACTGTATGTCTCTGTGAGAAATGGAATGCTCTTATTCAGCTGCAGCATGTGGTTGA 722
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 902 GTGTGAGCCCTTATCAGACACATTTGGGATCATGGAATGAGCCATCCCTGGGCGAG 961
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 723 GTGTGATGCTGTACAAATCCACCAATGAGGTGTGTGGAATGTTCCAAAACCTGTGAAG 782
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 962 CTTCACCTTACCTCTGATCTTCTTCACTGCTCTCAGAAAGAACTGATTAATTGGGAA 1021
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 783 CTTCCTCATGAAACAACCTGTACATTTGACTGTGAAGAAGATTTGAACATAATGGAGC 842
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1022 GAAGAAAACCAATTTGTGATCATCTGGAATCTGTCAATCTGATCCAAATATGTCA 1079
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DB 843 CCAGAGCCTTCACTGTACCTCATCTGTGGAATTTGGACAACGAGAAGCAACGTGTAA 900
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RESULT 14
US-09-209-668-18
; Sequence 18, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
```

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; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 3834
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (117)..(1949)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: M24736/Genbank
; DATABASE ENTRY DATE: 1994-11-07
US-09-209-668-18

Query Match      13.7%: Score 310; DB 3; Length 3834;
Best Local Similarity 60.6%: Pred. No. 4.3e-81;
Matches 508; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

QY 242 CTGGACTTACCATTTATCTGAAAAAACCATGAACTGGCAAGGCTTGAAAGATTCGCCG 301
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 179 ctggtcttaaacaccctcccgagactatgactatgactatgactatgactatgactatg 238
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 302 AGACAAATTAACAGATTTAGTGGCATACAAAACAGCGGAAATGATGTGAGAA 361
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 239 gcaaaagtlacacacactgltgcacttcaaaacaaagaagatgltgactcctcaaac 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 362 GACTCTGCCCTTACGTCGTTCTTACTACTGATAGAAATCCGGAAGTATGAGAGATATG 421
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 299 catactagctattcaccaagattacttgatttgaaatcagaagaatcagaatcagaat 358
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 422 GACTGTGGGTGGGAACCAAAATCTCTCACTGAAGAAGACAGAACTGGGAGATGGTGA 481
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DB 359 gtlctggtlagaagcccaagaacctctgacagaagaagccaagaacctggtccagtlga 418
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QY 482 GCCCAACACAAAGAACAGAGACTGCTGAGATCTATATCAAGAAACAAGA 541
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 419 acccaaaatcagaagaaagatgagactgcgtgagatctacatcagaagaaagaa 478
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 542 TGCAGGCAATAGGACGATAGCGCTGCCACAAACTAAAGCAGCCCTGTGTCACAGC 601
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 479 tgltygcatgtgaaatgatagagtlgcagaagaagaagcttcctatgtctacagagc 538
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QY 602 TTCTTGCCACCCCTGTGTCATGAGTGGCCATGAGAAATGTGTAGAAATCATATAATCA 661
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DB 539 tgcctgtaccaataacatcctcgtcagtlgcccagtlgtaagtlgtaagacatcaatla 598
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QY 662 CACTCTGCACTGTGATGTGGGGTACTATGGGCCCACTGTGACCTTGTGATTCAGTGTGA 721
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 599 caactlgaagtgtgaaacctgtgctcagtlgaactaaagtgtgagcaaatltgtgaactgt 658
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QY 722 GCCTTTGAGAGCCCAAGAGTGGGTATACATGAGTGTACTACCCCTTGGAAACTTCAG 781
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DB 659 agccctlgaatccctcgtgagatgagagcctgtgttgagtlcaaccacatcgtgaaactcag 718
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QY 782 CTTCACCTCAGAGTGTGCTTCTGAGCTGCTTGAAGGAACAACCTTAACTGGGATGAGA 841
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DB 719 ctcaaatcttccctcgtcctacagctltgataaggttactctgacagcagatgagac 778
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QY 842 AACCACTGTGGACATTTTGGAAACTGTATCTCCAGAAACAACCTGTCAAGTGAATCA 901
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DB 779 calygaagtgtatgtcctctcgtgagaaatgtgtccatcaccagcctgcaaatgtgtgtga 838
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QY 902 GTGTGAGCCCTTATCAGACACAGATTTGGGATCATGGAATGATGATCCCTGGGCGAG 961
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DB 839 gtlgtatgctgtgacaaatccagcgaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 898
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 962 CTTCACCTTACCTCTGATCTTCTTCACTGCTCTCAGAAAGAACTGATTAATTGGGAA 1021
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2001, 23:50:05 ; Search time 3458.26 Seconds

(Without alignments)
9652.488 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14155048 seqs, 7388405095 residues

Total number of hits satisfying chosen parameters: 28310096

Minimum DB seq length: 0
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Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
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2	2161	95.7	2354	US-09-023-655-1154	Sequence 1154, Ap
3	2151.6	95.2	2385	US-60-243-521-8	Sequence 8, Appl
4	2150	95.2	2385	US-60-213-360-1118	Sequence 1118, Ap
5	2150	95.2	2564	US-09-396-970-8480	Sequence 8480, Ap
6	2146.8	95.0	2385	US-09-495-050A-292	Sequence 292, App
7	2129.6	94.3	2387	US-60-118-318-292	Sequence 292, App
8	2087.6	92.4	2330	US-60-172-373-15742	Sequence 15742, A
9	2087.6	92.4	2330	PCT-US92-03970-1	Sequence 1, Appl
10	2087.6	92.4	2330	PCT-US94-00909-1	Sequence 1, Appl
11	2087.6	92.4	2330	US-08-008-459-1	Sequence 1, Appl
12	2087.6	92.4	2330	US-08-340-539-1	Sequence 1, Appl
13	2087.6	92.4	2330	US-08-410-569-1	Sequence 1, Appl
14	1605.4	71.1	1788	US-60-164-285-5139	Sequence 5139, Ap
15	1605.4	71.1	1788	US-60-164-285-5139	Sequence 5139, Ap
16	1006.4	44.6	3238	US-60-212-659-816	Sequence 816, App
17	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
18	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
19	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
20	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
21	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
22	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
23	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
24	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
25	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
26	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
27	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
28	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
29	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
30	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
31	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
32	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
33	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
34	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
35	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
36	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
37	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
38	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
39	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
40	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
41	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
42	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
43	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
44	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App
45	970.2	42.9	141589	US-09-543-679A-2480	Sequence 2480, App

ALIGNMENTS

RESULT 1
US-09-119-209-1

Sequence 1, Application US/09119209
GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: YEDNOCK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,209
FILING DATE: 20-Jul-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513278
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059027
FILING DATE: 6-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/315015
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0565D1C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2259 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-119-209-1

Query Match 100.0%; Score 2259; DB 15; Length 2259;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAGTGTGCTGCTTCTCACTGACACAGACACACTCCCTTGGCAAGACT 60
DB 1 GAATTCAGTGTGCTGCTTCTCACTGACACAGACACACTCCCTTGGCAAGACT 60
QY 61 GAGACCCCTTGCTGAAGCAAGGCTCAATGGGCTGAGAGAAACTGAGAGAGCA 120
DB 61 GAGACCCCTTGCTGAAGCAAGGCTCAATGGGCTGAGAGAAACTGAGAGAGCA 120
QY 121 GCAAGCCATGATATTTCCATGGAATGTCAAGAGCACCAGAGGACTTATGAACTCT 180
DB 121 GCAAGCCATGATATTTCCATGGAATGTCAAGAGCACCAGAGGACTTATGAACTCT 180

DB 121 GCAAGCCATGATATTTCCATGGAATGTCAAGAGCACCAGAGGACTTATGAACTCT 180
QY 181 TCAAGTTGTGGGGGTGACATATGCTGTGTGATTTCTGGACATCATGAACTACT 240
DB 181 TCAAGTTGTGGGGGTGACATATGCTGTGTGATTTCTGGACATCATGAACTACT 240
QY 241 GCTGACTTACCATTTATTTGAAAAAACCATGACATGCGAAGGCTAGAACTTCC 300
DB 241 GCTGACTTACCATTTATTTGAAAAAACCATGACATGCGAAGGCTAGAACTTCC 300
QY 301 GAGCAATTACACAGATTTGTTGCCATACAAAAGCGGAAATGAGTATCTGAGAA 360
DB 301 GAGCAATTACACAGATTTGTTGCCATACAAAAGCGGAAATGAGTATCTGAGAA 360
QY 361 AGACTGCCCCCTTCACTGCTTCTTACTAGTAGAATCCGAGATGAGAGAAAT 420
DB 361 AGACTGCCCCCTTCACTGCTTCTTACTAGTAGAATCCGAGATGAGAGAAAT 420
QY 421 GGAAGTGGGTGGGAGACCAAAATCTCTCACTGAGAAAGACAGAACTGGAGATG 480
DB 421 GGAAGTGGGTGGGAGACCAAAATCTCTCACTGAGAAAGACAGAACTGGAGATG 480
QY 481 AGCCCAACAAGAAAGAAAGAGAGAGACTGCGTATATATCAAGAGAAACAAG 540
DB 481 AGCCCAACAAGAAAGAAAGAGAGAGACTGCGTATATATCAAGAGAAACAAG 540
QY 541 ATGACAGCAAAATGAAAGATGACGCTGCGACAAACTAAAGGACCCCTGTTACACAG 600
DB 541 ATGACAGCAAAATGAAAGATGACGCTGCGACAAACTAAAGGACCCCTGTTACACAG 600
QY 601 CTTCCTGGCCAGCCCTGCTATGATGATGATGATGATGATGATGATGATGATGATG 660
DB 601 CTTCCTGGCCAGCCCTGCTATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 661 ACACCTGCAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
DB 661 ACACCTGCAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
QY 721 AGCCTTTGAGGCCCCAGAGCTGGGTATGATGATGATGATGATGATGATGATGATG 780
DB 721 AGCCTTTGAGGCCCCAGAGCTGGGTATGATGATGATGATGATGATGATGATGATG 780
QY 781 GCTTACGCTCAACAGTGTGCTTCACTGCTGTAAGAAACAACCTTAACTGGATGA 840
DB 781 GCTTACGCTCAACAGTGTGCTTCACTGCTGTAAGAAACAACCTTAACTGGATGA 840
QY 841 AAACCACTGTGAGACATTTGGAACCTGCTCATCTCAGAAACAACCTGTCAGTATTC 900
DB 841 AAACCACTGTGAGACATTTGGAACCTGCTCATCTCAGAAACAACCTGTCAGTATTC 900
QY 901 AGTGTAGCCTCTATCAGCAGCAGATTTGGGATCATGAACTGTAGCCATCCCTGGCCA 960
DB 901 AGTGTAGCCTCTATCAGCAGCAGATTTGGGATCATGAACTGTAGCCATCCCTGGCCA 960
QY 961 GCTTACGCTTACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
DB 961 GCTTACGCTTACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
QY 1021 AGAAGAAACCATTTTGTGATCATCTGGAATCTGTGCAAACTAGTCAATATGTCAAA 1080
DB 1021 AGAAGAAACCATTTTGTGATCATCTGGAATCTGTGCAAACTAGTCAATATGTCAAA 1080
QY 1081 AATTGCAAAAGTTTCTCATGATTTAAGAGGGTGTATTAAACCCCTCTCATATCCAG 1140
DB 1081 AATTGCAAAAGTTTCTCATGATTTAAGAGGGTGTATTAAACCCCTCTCATATCCAG 1140
QY 1141 TGGCAGTATGTTTACTGATCTCTGAGTTTGCATTTATCATTTTGGCTGCAAGAGAT 1200
DB 1141 TGGCAGTATGTTTACTGATCTCTGAGTTTGCATTTATCATTTTGGCTGCAAGAGAT 1200
QY 1201 TAAAAAAGGCAAGAAATCCAAAGAAAGTATGATGATGATGATGATGATGATGATGATG 1260
DB 1201 TAAAAAAGGCAAGAAATCCAAAGAAAGTATGATGATGATGATGATGATGATGATGATG 1260


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QY 1261 AAAGAAATCTTGGAATCTATAAATCATGAGATCTTTAAATCCTTCATGAACGTT 1320
Db 1261 AAAGAAATCTTGGAATCTATAAATCATGAGATCTTTAAATCCTTCATGAACGTT 1320
QY 1321 TTGTGTGGTGGACCTCCCTGCTCAACAAATGAAGTGTGCTTCCTTCATGATCGGGAG 1380
Db 1321 TTGTGTGGTGGACCTCCCTGCTCAACAAATGAAGTGTGCTTCCTTCATGATCGGGAG 1380
QY 1381 ATTTCTACCGGACCAACAGTTCCTTCAGCTTCATTCGCCCCCTCATTTATCCCTCAAC 1440
Db 1381 ATTTCTACCGGACCAACAGTTCCTTCAGCTTCATTCGCCCCCTCATTTATCCCTCAAC 1440
QY 1441 CCCAGCCCAAGAGTGTATATACAGCTCAGCTTTTGTCTTTTCTGAGAGAAACAATAA 1500
Db 1441 CCCAGCCCAAGAGTGTATATACAGCTCAGCTTTTGTCTTTTCTGAGAGAAACAATAA 1500
QY 1501 GACCATTAAGGAAAGATATATGTAATATAAGATGGCTGACCTTGTCTTTCTTGAC 1560
Db 1501 GACCATTAAGGAAAGATATATGTAATATAAGATGGCTGACCTTGTCTTTCTTGAC 1560
QY 1561 TCTGTGTTTCAGTTTCATTCAGTGTCTGATGATGACAGACACTTCTAAATGAAGTGC 1620
Db 1561 TCTGTGTTTCAGTTTCATTCAGTGTCTGATGATGACAGACACTTCTAAATGAAGTGC 1620
QY 1621 AAATTTGATACATATGTAATATGAGACTGTTTCTGACATCAAAATTTACAGTGTGC 1680
Db 1621 AAATTTGATACATATGTAATATGAGACTGTTTCTGACATCAAAATTTACAGTGTGC 1680
QY 1681 TTCTGTATACGTGAGAGTCACTCTATATGAAGTCAAAAGTCAAGCTCCCTTC 1740
Db 1681 TTCTGTATACGTGAGAGTCACTCTATATGAAGTCAAAAGTCAAGCTCCCTTC 1740
QY 1741 TTTCTACTCCATGAGTAATGAGGCTCTGCTCAAGTTGAAAGAGTCTATTTGCACTG 1800
Db 1741 TTTCTACTCCATGAGTAATGAGGCTCTGCTCAAGTTGAAAGAGTCTATTTGCACTG 1800
QY 1801 TACCTGCGCGCTGTGTAATGAGACCTCTATTTAACTGGCTTCAGGCTCCCACTT 1860
Db 1801 TACCTGCGCGCTGTGTAATGAGACCTCTATTTAACTGGCTTCAGGCTCCCACTT 1860
QY 1861 CTTCAGGACCTCTCTTTTTCAGTGGCTGACTCCACACTGACATCTCATGAGTCCA 1920
Db 1861 CTTCAGGACCTCTCTTTTTCAGTGGCTGACTCCACACTGACATCTCATGAGTCCA 1920
QY 1921 AGCAAAAGAGAGAGAGAGAAATAGCCTGCGGCTTTTATGTTGGGGTTTGTCTGT 1980
Db 1921 AGCAAAAGAGAGAGAGAGAAATAGCCTGCGGCTTTTATGTTGGGGTTTGTCTGT 1980
QY 1981 TTCTCTTTATGAGAACCCATTCCTATTTCTATATGTCATAGTCTTTTATACAGATATTA 2040
Db 1981 TTCTCTTTATGAGAACCCATTCCTATTTCTATATGTCATAGTCTTTTATACAGATATTA 2040
QY 2041 TTATGTAAGAAACATCTCTGAAATGCTAGTGCAGATGATCTCTTTGATGATATGG 2100
Db 2041 TTATGTAAGAAACATCTCTGAAATGCTAGTGCAGATGATCTCTTTGATGATATGG 2100
QY 2101 AAGAGTTAAAGAGGTGAGAGAAATTCCTGATTCACAATGCAATGCTCTCTTTCCCTG 2160
Db 2101 AAGAGTTAAAGAGGTGAGAGAAATTCCTGATTCACAATGCAATGCTCTCTTTCCCTG 2160
QY 2161 CCCCCAGAACTTTTATTCACATCTTACATGATTTCAATATTTCAATCTCAAGC 2220
Db 2161 CCCCCAGAACTTTTATTCACATCTTACATGATTTCAATATTTCAATCTCAAGC 2220
QY 2221 CTCCCTCAACCCGAGGCGCGCAGACACTGGAATTC 2259
Db 2221 CTCCCTCAACCCGAGGCGCGCAGACACTGGAATTC 2259
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RESULT 2
US-09-023-1154
; Sequence 1154, Application US/09023655

```
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1154:
SEQUENCE CHARACTERISTICS:
LENGTH: 2354 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g187182
US-09-023-655-1154

Query Match 95.7%; Score 2161; DB 14; Length 2354;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2200; Conservative 0; Mismatches 10; Indels 3; Gaps 3;

QY 25 ACCTGACAGCAGCAGCAGCTCCCTTTGGCAAGGACCTGAGACCTTGTGCTAAGTCAAGAG 84
Db 12 ACCTGACAGCAGCAGCAGCAGCTCCCTTTGGCAAGGACCTGAGACCTTGTGCTAAGTCAAGAG 71
QY 85 GCTCAATGGGCTGAGAGAACTAGAGAGGACCAAGCAAGCAATGATTTTCATGGA 144
Db 72 GCTCAATGGGCTGAGAGAACTAGAGAGGACCAAGCAAGCAATGATTTTCATGGA 131
QY 145 AATGTACAGAGCAGCAGAGGAGCTTATGAAACATCTTCAAGTTGTGGGGGTGAGCAATGC 204
Db 132 AATGTACAGAGCAGCAGAGGAGCTTATGAAACATCTTCAAGTTGTGGGGGTGAGCAATGC 191
QY 205 TCTGTGTGATTTCTGCGACATCATGGAACCTACTGCTGAGCTTACCATTTATTTCTGAAA 264
Db 192 TCTGTGTGATTTCTGCGACATCATGGAACCGAGCTGCTGAGCTTACCATTTATTTCTGAAA 251
QY 265 AACCATGAACTGGCAAAAGGCTAGAGATTCGCGAGAGCAATTTACAGAGATTTAGTTG 324
Db 252 AACCATGAACTGGCAAAAGGCTAGAGATTTCTCCGAGAGCAATTTACAGAGATTTAGTTG 311
QY 325 CCATACAAACAAAGCGGAAATTTGATATCTGGAAGACTCTGCCCTTCAGTGTCTTCTT 384
Db 312 CCATACAAACAAAGCGGAAATTTGATATCTGGAAGAGACTCTGCCCTTTCAGTGTCTTCTT 371
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QY	1464	GCTCAGCTTTTGTCTTTTCTGAGAGAAAACAATAAGACAT - AAGGGAAAGGATTCAT	1522
Db	1452	GCTCAGCTTTTGTCTTTTCTGAGAGAAAACAATAAGACATTAAGACATTAAGGGAAAGATTCAT	1511
QY	1523	GTGGATATATAAGATGCGTCAGCTTTGGCTCTTCTTGATCTTGTTTTCAAGTTCAATTTCA	1582
Db	1512	GTGGAAATATAAAGATGCGTCAGCTTTGGCTCTTCTTGATCTTGTTTTCAAGTTCAATTTCA	1571
QY	1583	GTGCGTACTGTGATGACAGACACTCTTAATGAAAGTGCAAATTTGATACATATGTGATA	1642
Db	1572	GTGCGTACTGTGATGACAGACACTCTTAATGAAAGTGCAAATTTGATACATATGTGATA	1631
QY	1643	TGGACTCAGTTTCTTGTGCAGATCAAAATTTACGCTCTTCTTGATCTGATAGTGGAGTACA	1702
Db	1632	TGGACTCAGTTTCTTGTGCAGATCAAAATTTACGCTCTTCTTGATCTGATAGTGGAGTACA	1691
QY	1703	CTCTTATGAAAAGTTCAAAAAGTCACGCTCTCTCTTTCTTCTTCAACTCCAGTGAAGTAT	1762
Db	1692	CTCTTATGAAAAGTTCAAAAAGTCACGCTCTCTCTTTCTTCTTCAACTCCAGTGAAGTAT	1751
QY	1763	GGGGTCGCGTCACAGTTGAAAAGTCCATTTGACATGATAGCTCGCGCTCGTGAATG	1822
Db	1752	GGGGTCGCGTCACAGTTGAAAAGTCCATTTGACATGATAGCTCGCGCTCGTGAATG	1811
QY	1823	GACCATCTATTTAACGTGGCTCAGGCTCCGCCACCTTTTGAGCCACCTCTCTTTTCA	1882
Db	1812	GACCATCTATTTAACGTGGCTCAG - GCGTCCGCCACCTTTTGAGCCACCTCTCTTTTCA	1870
QY	1883	GTGGCTGACCTTCCACACCTAGATCTCATGATGTGCAAGCAAGAAAAGAGAGAGAGAA	1942
Db	1871	GTGGCTGACCTTCCACACCTAGATCTCATGATGTGCAAGCAAGAAAAGAGAGAGAGAA	1930
QY	1943	ATAGGCTGCGCGGTTTTTATGTTGGGGGTTTTGGCTGTTCTTTTATGAGAACCATTTCC	2002
Db	1931	ATAGGCTGCGCGTGTTTTTATGTTGGGGGTTTTGGCTGTTCTTTTATGAGAACCATTTCC	1990
QY	2003	TATTTCTTATATGTCATGTCTTTTATATCAGATATTTATAGTAAGAAACATCACTGAA	2062
Db	1991	TATTTCTTATATGTCATGTCTTTTATATCAGATATTTATAGTAAGAAACATCACTGAA	2050
QY	2063	ATGTCTACTCGAAGTGCATCTCTTTGATGTGTCATATGGAAGGTAAAGAGTGGAGAA	2122
Db	2051	ATGTCTACTCGAAGTGCATCTCTTTGATGTGTCATATGGAAGGTAAAGAGTGGAGAA	2110
QY	2123	ATTCCTTGATTCACAATGAATGCTCTCTCCCTCCCGTCCCGCCAGAACCTTTATCACTT	2182
Db	2111	ATTCCTTGATTCACAATGAATGCTCTCTCCCTCCCGTCCCGCCAGAACCTTTATCACTT	2170
QY	2183	ACCTAGATTCACATATTCCTTAATAATTATCTCAGGCTCCCTCAACCCAC	2235
Db	2171	ACCTAGATTCACATATTCCTTAATAATTATCTCAGGCTCCCTCAACCCAC	2223
RESULT 3			
US-60-243-521-8			
Sequence 8, Application US/60243521			
GENERAL INFORMATION:			
APPLICANT: Hopkins, Christopher M.			
APPLICANT: Peterson, David P.			
APPLICANT: Cocks, Benjamin G.			
APPLICANT: Hawkins, Phillip R.			
TITLE OF INVENTION: GENES REGULATED IN ACTIVATED T CELLS			
FILE REFERENCE: PA-0042 P			
CURRENT APPLICATION NUMBER: US/60/243, 521			
CURRENT FILING DATE: 2000-10-25			
NUMBER OF SEQ ID NOS: 116			
SOFTWARE: PERL Program			
SEQ ID NO 8			
LENGTH: 2385			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: misc_feature			

OTHER INFORMATION: Template ID: 331616.2
US-60-243-521-8

Query Match 95.2%; Score 2151.6; DB 56; Length 2385;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2201; Conservative 0; Mismatches 9; Indels 4; Gaps 4;

25 ACCTGCACGACGACACACTCCCTTTT-GGCAAGACCTGAGACCCCTGTGCTAAAGTCAAGA 83
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32 acctgcagacagacacactccctcttgagcaagaccctgagacccttgctaaagtcaga 91
84 GGCTCATGCGCGCGAAGAACTAGAGAGAGCAAGCAAGCCATGATATTCATG 143
92 ggtcctaatggcgcgcagaaagaaactaagaaagaaagcaagcaatgatalctcaatg 151
144 AATGTCTAGAGACCCAGAGAGGACTTATGAGACATCTTCAAGTGTGGGGTGGACAAATG 203
152 aaatgctagagacccagagagactatgaaacatctcaagtctgggggtagacaatg 211
204 CTCTGTTGTGATTTCTCGGCACATCATGACACTGCTGACCTTACATTAATCTGAA 263
212 ctctgtgtgtattcttcgacacatcagaccgactgctgacttaccatctctcgaa 271
264 AAACCATGAACTGGCAAGGGCTAGAGATTCGCGGAGACAAATTAACAGATTTAGTT 323
272 aaaccatgaaacgcgcagaaaggtcagaagaatctgcgcgagaacaatlaacagatctagtc 331
324 GCCATCAAAACAAAGCGGAAATTTGATATCTGAGAAAGACTGCGCTTCAGTCTCT 383
332 gcaatacaaaacaagcgcgaatctgactctggagaaagctctgccttcagtcgtctc 391
384 TACTACTGATAGGAATCCGGAAGATAGAGAAATGACGTTGGTGGGACCAACAA 443
392 tactactgtagaagaaaccgcgaagatagagaaatagatgagcgtggtggaacaaacaa 451
444 TCTCTAGTGAAGAGAGAGAACTGGGGAGATGTGAGGCCCAACAAAGAGAAAGCAAG 503
452 tcccttaactgaaagaaacagagaaactcgaggagatcgtagaccacaacaaagaaagaaag 511
504 GAGAGCTGCGTGGAGATCTATATCAAGAGAAACAAAGATGACAGCAAAATGGAAGATGAC 563
512 gagagactcgtagagatctcatcaagaagaaacaagaatgcaagcaaatgaaacgaatgac 571
564 GCCTGCCAACAACTAAAGGACCCCTCTGTTACACAGCTTCTTGCCAGCCCTGCTATGC 623
572 gctctgcacaacaaactaaagcagccctctgttacaacagctcttcgcagccctgtctatgc 631
624 AGTGGCATGGAAGATGTGTAAGAAATCATCAATCAACACCTGCAACTGTGATGGGG 683
632 agtggcacaagaaatgtaaaatcaatcaatcaatcaacccctgcaactgtagtgggg 691
684 TACTATGGGCCCCAGTGTGAGCTTGTGATTCAGTGTGAGGCTTGGAGGCCCCAGAGCTG 743
692 tactatgggcccagtgctcaagcttgtagatcaagtgtgagagcctcttgagagcccagagctg 751
744 GGTAACATGAGACTGTACTACCCCTTTTGGAACTTCAAGCTTCAAGCTCACAGTGTGCCCTTC 803
752 ggtacaatgtagctgtactaccctcttgaggaaacttcagcttcagctcaacgtgtgaccttc 811
804 AGTGTCTGTAAGGAACAACTTAAGTGGGATTTGAAGAAACACCTGTGACACATTTTGA 863
812 agtgtctctgaaagaaacaaacttaactgagatctgaaagaaacacacgtgtgaaacatltgga 871
864 AACTGTGATCTCTCAGAACCAACCTTGCAAGTATTCAGTGTGAGGCTCTATACAGACCA 923
872 aactgtgcatctctccaaacaaacacgtgcaagtgatcagtgtagcgtccatcaagaccaca 931
924 GATTTGGGATCATGAATGTGTAGCCATCCCTTGCCAGCTTCAAGCTTACCTGTGATGT 983
932 gatttgggatactgaaactgtagcatcccttgccagcttcagcttactctctgcacgtc 991
984 ACCTTATCTGCTCAGAAAGAACTGAGTTAATTGGGAAGAAAGAAACCATTTTGTGAATCA 1043

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992 accctcaatcgtctcagaagaagaaactgagtaatttgggagaagaagaaccatcttgtaatca 1051
1044 TCTGGAATCTGTGTCAAATCTAGTCAATATGTCCAAAATTTGACAAAGTTTCTCATAG 1103
1052 tctggaaatctggtcaaaatccctagtcacaatagtccaataattgagcacaagcttctcaatg 1111
1104 ATTAAGAGAGGTGATTTTAACCCCTCTTCAATTCAGTGCAGTCATGTTACTGCAATTC 1163
1112 attaaagagggtgattataaaccctctcattcaatgagtcagtcagtcagtcagtcagtc 1171
1164 TCTGGTTGGCATTTATCATTTTGGCTGGCAAGGATTTAAAGGATTTAAAGGCAAAATTCAG 1223
1172 tctgggttgcatcttaacatcttgctgcaagagatlaaaaaaagcaagaaatccaaag 1231
1224 AGAAGTATGATGACCCCATATTAATGCGCCCTTGCTGTAAGAAATTTCTTGAATACTAA 1283
1232 agaagtagatgagcccatatlaaatcgcccttggtgaagaaatctcttgaaactactaa 1291
1284 AATATCATGAGATCCTTTAAATCCTTCATGAAACGTTTGTGTGTGGACACTCTCTACGT 1343
1292 aaatcaatgagatcccttaaaatccctcactcaatgaaagcttctgtgtgtgtgtgtgtgt 1351
1344 CAAACATGAAGTGTG-TTCCCTTCAGTGCATCTGGGAGATTTTACCCGACCAACAGTTTC 1402
1352 caaaacatgaaagtgtgtctccttcacagtcacatctggaagaatctcactcagacaagcttc 1411
1403 CTTCAGCTTCATTTGCGCCCTCATATTTATCCCTCAACCCCGACGCCACAGTGTATTAC 1462
1412 cttaagcttccatcttgccctccatcttatccctcaaccccgacagctgtgttatac 1471
1463 AGCTCAGCTTTTGTCTTTTCTGTGAGGAGAAACAAATTAAGACCAT-AAGGGAAAGGATTCA 1521
1472 agctcagcttctgtctctctctgagagaaacaataagacataagaggaagaaagatctca 1531
1522 TGTGGAATTAAGAAAGTGAAGTGTGACTTTGCTCTTCTTACACTTGTGTTCAATTC 1581
1532 tgtggaataaagaatgagcgcgaactctctctctctctctctctctctctctctctcaatctc 1591
1582 AGTGTCTACTTGTATGACAGACACTTCTTAATGAAGTGAAGTGAATGTATATGTGAAT 1641
1592 agtgcgtactctgtagtcagacactctctaataatgaaatgaaatctgtatcatatgtgaatc 1651
1642 ATGACATCACTTTTCTTGTGAGATCAAAATTTACAGTCTGCTTCTGTATATCTGTGAGATAC 1701
1652 atgacatcaatcttctctgagatcaaaatctcaacgtctctctctctctctctctctctctct 1711
1702 ACTCTTATGAAGAAAGTTCAAAAAGCTACGCTCTCTCTTCTTCTTCACTCCAGTCAACTAA 1761
1712 acccttaabagaagatcaaaaaagctcagctcctctctctctctctctctctcaatccagtgaa 1771
1762 TGGGGTCTCTCTCAAGTTGAAGAGTCTATTTGTCACTGTAGGCTCGCTCTGTGTAAT 1821
1772 tggggctctctctcaagtgtagaagagctctatcttgcaactgtgacgtcgtctgtgaaatc 1831
1822 GGACATCTCTATTTAACTGTGCTTCAGGCTTCGCCACCTTCTTACGCCACCTCTCTTTTTC 1881
1832 ggaacatctctatcttaactgtgcttca-gcctcccaacctctctcaagcaacctctctcttc 1890
1882 AGTTGGCTGACTTCCACACCTAGACCTCATGAGTGTGCAAGGCAAAAGAGAGAGAGAGA 1941
1891 agttggctgactctccacaacctagacatccatgagtcgcaagcaaaagagagaagagaga 1950
1942 AATAGCTGCGCGGTTTTTTAGTTTGGGGGTTTTTGTGCTTCTTCTTATAGAACCAATTC 2001
1951 aatagctcgtgcgtcttcttaagtttgagggttctgctgtctctcttcttaagagaccatctc 2010
2002 CTATTTCTTAATGTAATGTTTCTTTTATACAGATATTAATTAAGAAACATCACTGA 2061
2011 ctattctctatagcaatgtctctcttatacagatataatagtaagaaacaatcaactgaa 2070
2062 AATGCTAGCTGCAAGTGAACATCTTGTGATGTCAATATGGAAGGATTTAAACAGGTGAGAGA 2211
|||||


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Db 1592 agtgcgtactgtatgacagacactcttaaatgaagtcgaatttgtatcatatgtagat 1651
      |||
Qy 1642 ATGACATCAGCTTTCTTTCGACATCAATTTACACTGCTCTTCTGTATACCTGAGAGTAC 1701
      |||
Db 1652 atggaacacagcttctgcagatcaaatltcaagctgtcttcttcttcaatctgtagagtag 1711
      |||
Qy 1702 ACTTTTATGAAAGTCTCAAAAGTCTACGCTCTCTTCTTCTTACCTCCAGTGAAGTAA 1761
      |||
Db 1712 acctctatagaagaagtcataaaagctcaagctctctcttcttcttcaatctcaagtcagtag 1771
      |||
Qy 1762 TGGGGCTCTGCTCAAGTTGAAAGAGTCTATTTTGCACCTAGTACCTCGCGCTGTGTGAAT 1821
      |||
Db 1772 tggggctctgctcaagtcgaagtccttcttcttcttcttcttcttcttcttcttcttcttct 1831
      |||
Qy 1822 GGACCATCCTATTTAACTGGTTTCAGGCTCCGCCACCTTCTTCAAGCCACCTCTCTTTTTC 1881
      |||
Db 1832 ggaacatccatttcaatgtgtca-gctcccaaccttcttcttcttcttcttcttcttcttct 1890
      |||
Qy 1882 AGTGGCTGACTTCCACACCTAGCATCTCATGAGTGCACAAAGAGAGAGAGAGA 1941
      |||
Db 1891 agttggtgacttccacaacctagatcatgagtcgaagcaaaagagagagagagagagagagag 1950
      |||
Qy 1942 AATAGCTGCGCGGTTTATGTTGGGGGTTTGTCTGTTTCCTTTATGAGACCATTC 2001
      |||
Db 1951 aatagcctgcgctgttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 2010
      |||
Qy 2002 CTATTTCTTATAGCAATGTTTCTTTATACGATATTTATTTAGTAAAGAAACATCACTGA 2061
      |||
Db 2011 ctatcttctatagcaaatgttcttcttcttcttcttcttcttcttcttcttcttcttcttct 2070
      |||
Qy 2062 AATGCTAGTGCAGTACATCTCTTGTATGTCTATGATGAAAGATTTAAACAGGTGAGGA 2121
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Db 2071 aatgctagctgcgaagtcgacacctcttcttcttcttcttcttcttcttcttcttcttcttct 2130
      |||
Qy 2122 AATTCCTGATTCAATGAATGCTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2181
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Db 2131 aatctctgtcttcaaatgtgaatgtctctcttcttcttcttcttcttcttcttcttcttcttct 2190
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Qy 2182 TACCTAATTTCTACATTTCTTTTAAATTTCACTCAGAGCTCTCTCAACCCAC 2235
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Db 2191 taactagatctcatatcttcttcaatcttcaatcttcaatcttcaatcttcaatcttcaatct 2244
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RESULT 5
US-09-396-970-8480
; Sequence 8480, Application US/09396970
; GENERAL INFORMATION:
; APPLICANT: Kingsbury, David P.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: MLN98-40PA
; CURRENT APPLICATION NUMBER: US/09/396,970
; EARLIER FILING DATE: 1999-09-14
; EARLIER APPLICATION NUMBER: 60/100,293
; NUMBER OF SEQ ID NOS: 8756
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8480
; LENGTH: 2564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2564)
; OTHER INFORMATION: n = A,T,C or G
US-09-396-970-8480
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Query Match 95.2%; Score 2150; DB 17; Length 2564;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2200; Conservative 0; Mismatches 10; Indels 4; Gaps 4;

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Qy 25 ACTGCACACAGCAGCACTCCCTTT-GGCAAGAGACTGAGACCCCTTGTGCTAAGTCAAGA 83
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Db 50 aactgcagacagacacactcccttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 109
      |||
Qy 84 GGTCTCAATGGGCTGAGAAAGTATGAGAGAGACCAAGCAAGCCATGATATTTCCATAGC 143
      |||
Db 110 ggtctcaatgggctgcagagagacttagagagagcaagcaagcaatgatatcttccatg 169
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Qy 144 AATATGTAGACACCCAGAGAGACTTATGAAACATCTTCAAGTTGTGGGGTGCACATG 203
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Db 170 aatattcagagacacccagagagacttagagagacatcttcaagttgttgggggtgcagaaatg 229
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Qy 204 CTCTGTTGATTTCTCTGACATCATGATGAACTCTCTGACTGTACCTATTTATCTTAA 263
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Db 230 ctctgtgtgttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 289
      |||
Qy 264 AAACCCATGAATGGCAAGGGCTAGAAATTTGCGGACAAATTTACAGATTTAGTT 323
      |||
Db 290 aaacccatgaacttgcgaagagcttagagagatcttgcgagacaattacagagatttagt 349
      |||
Qy 324 GCCATCAAAAACAAAGCGGAAATGATATCTGGAAGAACTGTGCTTCACTGCTTCT 383
      |||
Db 350 gccatcaaaaacaaagcggaatgtagatcttgcgaagaaacttgccttcaagtcgttct 409
      |||
Qy 384 TACTACTGATAGGAATCCGGAAGTATGAGAGAAATGAGAGTGGGTTGGAACCAACAA 443
      |||
Db 410 tactactgtagagaaatccggaagtagagaaatagagagtgagggtgggtgcgaacaa 469
      |||
Qy 444 TCTCTCATGGAAGACAGAGAACTGGGAGATGTTGGGCCCAACAAACAAAGAACAG 503
      |||
Db 470 tctcttactgtagaagacagagaaacttgcgagagatgtgtgagcccaacaaagaaagaaag 529
      |||
Qy 504 GAGAGCTGCTGAGATATATCAAGAGAAACAAAGATGCAAGCAATGGAACGATGAC 563
      |||
Db 530 gagagactcgtgcgagatctatatacaagaaacaaagtgcgaagcaaatgtgaacgatgac 589
      |||
Qy 564 GCGTCGCAAACTAAAGGCGCCCTGTGTACACAGCTTGTGCGACGCTGTGTCATGAC 623
      |||
Db 590 gccgcgcaaaactaaagcgagccctcttcttcttcttcttcttcttcttcttcttcttcttctt 649
      |||
Qy 624 AGTGCCATGAGAGATGTATGAATCATATCAATATCAACACTGCAACTGTGATGTGGG 683
      |||
Db 650 agtgcgcatgtagaagatgtgtagaaatcatcaatatactacacttgcgaactgtgagtggg 709
      |||
Qy 684 TACTATGGGCCCCAGTGTACGTTGTGATTCAGTGTGAGCCCTTGGAGCCCCAGAGCTG 743
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Db 710 tactatgggccccagtgtagtctgtgttgcagtgtagtgcgcttgcgagccccagagctg 769
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Qy 744 GGTACCATGAGACTGTACTACCCCTTTGGAAACTTCAAGCTTCACTGACATGTGCCCTTC 803
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Db 770 ggtaccatgagactgtactcaccccttgcgaaacttcaagcttcaagctcagtgcccttc 829
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Qy 804 AGCTGCTCTGAAAGAACAACTTAAGTGGAGTTGAAGAAACACACTGTGGACCAATTTGGA 863
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Db 830 agctgcctctgaaagaaacaaacttaacttgcgagatgtgaagaaacacacttgcgacatttgg 889
      |||
Qy 864 AACTGTGATCTCCAGAACCAACTGTCAAGTGTAGTGTGAGCCCTTATGACAGACCA 923
      |||
Db 890 aactgtcatctccagaaacaaactgtcaagtgtatcagtgtaggccttatacgaacca 949
      |||
Qy 924 GATTTGGGATCATGAAGTGTAGCCATTCCTGGCCAGCTTCACTTACTCTGCATGT 983
      |||
Db 950 gatttgggatactgaacttgaacatcccttgcgagcttcaagcttcaactcgcagctgtc 1009
      |||
Qy 984 ACTTTCATCTGCTCAGAAAGAACTGAGTTAATTTGGAAGAAAGAAACCAATTTGTAATCA 1043
      |||
Db 1010 accttcaatctgcagagagagacttagttaaatttggagaaagaaacacatttgcgaatca 1069
      |||
Qy 1044 TCTGGAATCTGTCAAAATCTAGTCAATATGTCAAAAATTTGACAAAGTTTCTCAATG 1103
      |||
Db 1070 tctggaatctgttcaaatctcagtcacaatgtatgcaaaaatgtgcacaaagttctcattg 1129
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Qy 1104 ATTAAAGAGAGGTGATTTAAACCCCTCTTCATTTGCAGTGGCAGTCATGTTACGCAATTC 1163
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[illegible]

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Db      2209  taccaagattccaatatctttaattcaattcgaagcctccccaacccac 2262

RESULT      6
; US-09-495-050A-292
; Sequence 292, Application US/09495050A
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATE
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: 2000-01-31
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 292
; LENGTH: 2385
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1876370CB1
; US-09-495-050A-292

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Query Match	95.0%;	Score 2146.8;	DB 18;	Length 2385;
Best Local Similarity	99.3%;	Pred. No. 0;		
Matches 2198;	Conservative 0;	Mismatches 12;	Indels 4;	Gaps 4

QY	25	ACCTGAGACAGACACACTCCCTTT--GCGAAGGACCTGAGACCTTGTGTTAAAGTCAGA	83
Db	32	acctgcagcaagaagacaactccctcttgggaagaagacctgagacccttgyctaagtcgaag	911
QY	84	GCGCTAAAGGGCTCCACAAACAACTAGAGGAAGGCCAAGCAAGGCCATGATATTTCCATG	144
Db	92	ggctcaatgggctgcagaagaactagaagaagccaagccaagccaagatattccatctg	151
QY	144	AAATCTGAGAGCACCCAGAGGAGCTTATGGAACATCTTCAAGTTGTGGGGTGGACAAG	201
Db	152	aaatgcagagcaccacagagggacttatgaaactcttcaagtctggygggtggaacaatg	211
QY	204	CCTGCTGTGATTTTCCCTGGCACATTCATGGAACCTACTCTGTGACTTTCCTTAA	261
Db	212	ctctgtctgtgcttccctgagacatcttggaaccgactgctgacttaccattcttcga	271
QY	264	AAACCATGAACTGGCGAAAGGGCGCTAAAGATCTCCGAGACATTTACAGATTTAGTT	321
Db	272	aaaccatgactcggcaaaagggtctgaagaatcttcgcgagacaattcacagattagct	331
QY	324	GCATACAAAACAAAGCGCGAAATTGATATCTCGAAGAGACTGTGCCCTTCACTCGTTCT	381
Db	332	gcatacaaaaacaagcgggaattgattatctlvgagaagactcvtcccttcagtgctct	391
QY	384	TACTACTGATAGGAATCCGGAAGATAGGAGGAATATGGAGCTGGGGTGGGAACCAACAA	441
Db	392	tactactggtatggaatcccgagaagataggaaggaatacggagcgtgggtgggaaccacaa	451
QY	444	TCTCTACTGAAGACGAGAACTGGGGAAGATGGTAGGCCCAACAAAGAAAGAAACAG	501
Db	452	tcctctactgaagaagcagagactcggggagatgtagcgcacaacaacaagaagaacag	511
QY	504	GAGAGCTGCCTGGAGATCTATATCAAGGAAACAAAGATGCAGGCAATGAGACGATGAC	561
Db	512	gaagactcgtcttgagatctatacaagaagaaacaagaatgcagccaatgysaagatgac	571
QY	564	GCCGCGCACAACTAAAGCGAGCCCTCGTTTACACAGCTTCTTGGCAGCCCTGGTCATGC	621
Db	572	ggtctgcacaacaactaagaagcagccctcgtttacacagctcttgcagcccttgcatagc	631
QY	624	AGTGGCCATGGAATGTGTGAATCATCATTAATATCACACCTGTCAACTGATGTATGGGG	681

Db	632	agtggccatgaggaaatgctgagaaacacacaaataataataactctgcaactctgtaatgtagg	691
Oy	684	TACTATGGGCCCCAGTGCAGCTTGATTTCACTGTGAGCCCTTTGGAGGCCCCAGAGCTG	743
Db	692	tactatggcccccaagtctcaagttctgtaattcagtgtagcctcttgaggcccccaagctg	751
Oy	744	GGTACATGAGACTGTACTCACCCCTTTGGAACTTAGCTTAGCTCACAGTGTGCCTTC	803
Db	752	gttaccatggaactgtactccacctctgggaagaactcagcttcagctcacaagtgtgcttc	811
Oy	804	AGCGCTCTGGAAGAACAACTTAACGTGGATTTGAAGAAACCAACCGTGGACACTTTTSGA	863
Db	812	agctgcctctgaaggaaacaacttaactcggatctgaagaacaacctgtgaccatttgyga	871
Oy	864	AACGTGCATCTCCAGAACCAACCTGTCAAGTATTTCACTGTGAGCCCTTATCACACCA	923
Db	872	aactggtcacctccagaaccaacaacctgtcaagtattcagtgtaggcctctatcagcacca	931
Oy	924	GATTTGGGATCATGAACCTGTAGCCATCCCTGTGGCCAGCTTGACCTTACCTCTGCATGT	983
Db	932	gatttgggatacatgaaactgtagcaatccccgtgcccagcttcagcttbaacctctgacgt	991
Oy	984	ACCTTCATCTGCTCAGAAAGAACTGAGTTAAATTGGGAAAGAAACCACTTTGTGATCA	1043
Db	992	accttcatctgctcagaagaagaactgttaattggaagaagaagaaacaactctgtgaatca	1051
Oy	1044	TCTGGAACTCGTCAAAATCCTAGTCCCAATATGTGCAAAATTTGCACAAAAGTTTCTCAATG	1103
Db	1052	ctgtgaatctggtccaaatccctgatacattgtccaaatgtgcataaacttgcgaagtctccaa	1111
Oy	1104	ATTAAAGAGGGTGATTTAAACCCCTCTTCATTTCCAGTGGACATGGTTACTGCATTC	1163
Db	1112	attaagagggtgataataaaccccccttcaatctccagtgtagcatgttactgtcattc	1171
Oy	1164	TCTGGGTGGCATTTATCATTTTGGCTGGCAGAGATTTAAAAAAGCGAAGAAATCCAG	1223
Db	1172	tctgtgttgatcattcaattcatttgcctgaggaagagattlaaaaaaggaagaaatcccaag	1231
Oy	1224	AGAAGTATMGATGACCCATTTAAATCGCCCTTGAGGAAGAAATTCGTGGAAATCA	1283
Db	1232	agaaagtatgaatgccccataatcaacgcctctgtggaagaagaatctctgtgaatacctaa	1291
Oy	1284	AAATCATGAGATCCTTTAAATCCTTCATGAAACGTTTGTGTGGTGGACCTCCTCACT	1343
Db	1292	aaatcatgagatccctttaaactcccttccatgaaagcttctgtgtgtagacctcctaagt	1351
Oy	1344	CAAAACATGAAGTGTG-TTCTTCAATGTGATCTGGGAAGATTTTCAACCCGACCAACATGTC	1402
Db	1352	caaaacatgaagtgttcttccctcctcagtcagtcagtcggaagattctctacccgacaaacagcttc	1411
Oy	1403	CTTGAGTTCATTTGGCCCCCTCAATTTATTCGTCMAACCCCGACCCCAAGGTGTTATAC	1462
Db	1412	cttcaagcttccattctgcccccttcaattacccctcaaccccccaagccaaagtgattatcc	1471
Oy	1463	AGCTCAGCTTTTGTCTTTCTGTAGAGGAAGAAACAAATTAAGACCAT-AAAGGAAGAGATCA	1521
Db	1472	agctcagccttctgtcttctctcgtgagggaacaaataagaacataaagggaaggaattcca	1531
Oy	1522	TGTGGATATTAAGATGGCTGACTTTGTCTTCTTGTGACTCTGTGTTTCAAGTTCAATTC	1581
Db	1532	tgttgaataataaagaatgctgcaactctgtccttctctgtaacctctgttccagtttcaatcc	1591
Oy	1582	AGTGCCTACTGTGATGACACACACTTAAAGAAAGTGAAGTGAATTTGATATCAATGTGAAT	1641
Db	1592	agtgctgtaactgtgacgagacacactctcaatggaagtgcacaaattctgatacacaatgtagat	1651
Oy	1642	ATGAGCATGAGTTTCTTGACGATCAAAATTTCAAGTGTCTTGTATACTGTGAGAGTAC	1701
Db	1652	atggaacctagtttctctgtagaatcaaatccaagctgcgtctctctgtatatactgtgtagagctac	1711
Oy	1702	ACTGTATAGAAAGTTCAAAAAGCTTACGCTCTCCTTCTTCTAATCTCAGTGAAGTAA	1761

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Db      1712  actctatagaagaagtcataaaagtcacgcctcctctctcttcttcttaaccacagtgaaagtaa 1771
Oy      1762  TGGGGTCCCTGCTCAAGTTGAAAGAGTCCCTATTTTGGCACTGTAGACCTCGCCGTCTGTAATT 1821
Db      1772  tggggctccgtcctcaagtcgtgaaagagtcctatttgcactgtagccgcgcgtctgtaact 1831
Oy      1822  GGACCATCCCTATTTAACGTGCGCTTCAGGCGCTCCCAACCTTCTTTACAGCCACCTCTTTTTC 1881
Db      1832  ggcaccatccatttaaccggtctca-gcctcccaacctctcttcagccaacctcttcttc 1890
Oy      1882  AGTTGCTGACATCTCCACACCTAGACATCTCATGAGTGGCCAAACAAAGAGAGAGAGAGA 1941
Db      1891  agttgcgcgaactcccaaccacccatcccaagagtgcacaagaaagagaaagagagaga 1950
Oy      1942  AATAGCCGCGCGGGTTTTTTTATGTTTGGGGGTTTGTCTGTTTCTTTTATGAGACCCATTTC 2001
Db      1951  aatagccgcgcgtgttttttagtttagtttgggggttttgctgtcttccctttatgtgaccattc 2010
Oy      2002  CTATTTCCTTAATAGTCAATGTTTCTTTTATTCACGATATTATTATGATAGAAAACATCACTGA 2061
Db      2011  ctattcttatagtcaaatgattctcttcttcaagatatattagtaagaaacacatcactga 2070
Oy      2062  AATGTTACTCGAATGATGACATCTCTTTGATGTCATGTCATGATGAGAGAGTTAAACAGGTGGAGA 2121
Db      2071  aatgctagctgaagatgacacatcctcttgatgcatatagaagatctaaacagaagtcgaga 2130
Oy      2122  AATTCCTTGATTTCAACAAGAAATGCTCTCTCTTTCCTTCCTCCGCCCCAGAACTTTTATCCACT 2181
Db      2131  aattccttgattcacaagaagaaatgctctcctcttccctccgcgccacgaactttatccact 2190
Oy      2182  TACCTAGATTCTCAATATTCTTTTAAATTTCATCTCAGGCGCTCCCTCAACCCAC 2235
Db      2191  taccatgattctacatattctttaattcatctcaagcctccctcaaacccac 2244

RESULT 7
US-60-118-318-292
; Sequence 292, Application US/60118318
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATE
; FILE REFERENCE: PA-0013 P
; CURRENT APPLICATION NUMBER: US/60/118, 318
; CURRENT FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: PERL Program
; SEQ ID NO 292
; LENGTH: 2385
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: _
; OTHER INFORMATION: 187637OCBI
US-60-118-318-292

Query Match          95.0%: Score 2146.8; DB 43; Length 2385;
Best Local Similarity 99.3%: Pred. NO. 0;
Matches 2198; Conservative 0; Mismatches 12; Indels 4; Gaps 4;

Oy      25  AACTGACAGACAGCAGCACTCCCTTT-GGCAAGGAGCTGAGACCTGTGCTAAGTCAAGA 83
Db      32  aactgacagacagcagcactcccttggcgaagcctgagaccccttggcctaagtcaga 91
Oy      84  GGCTCAATGGCGCTGCAGAGAACTAGAGAGAGACCAAGCAAGCCATGATATTTCATGG 143
Db      92  ggctcaatggcgtcgaagaagactagagaagaccaaagccatgatatcttcacatgg 151
Oy      144  AAATGTCAGACACCCCAAGGAGCTTATGSAACATCTTCAAGTTGTGGGGTGTGACATG 203
Db      152  aaatgctcagacaccccaagaggactatggaacatcttcaagtcgtgggggtggaacatg 211

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204 CTCGTGTGATTTCTGGCACATCATGGAACCTTACTGCTGGACCTTACCATTTATCTGAA 263
|||||
Db 212 cctctgttgatcttccttgcgcacatactggaacccgactctggaacttaccatattctgaa 271
QY 264 AAACCCATGAGACTGGCAAAAGGGCTGAAGATTCTGCCGAGAACAAATTACAGATTAGTT 323
Db 272 aaaccacgaactcgtgcaaaagcctagaagattctgcgagaacaattacacagatttagt 331
QY 324 GCCATGCAAAACAAAGGGGAAATTGATGATCTGGAGAGACTCTGCCCTTACAGTCTCT 383
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Db 332 gccatacaaaaagcggaaacttgagtaacctggagaagactctgaccttcaagtcttct 391
QY 384 TACTACTGATAGGAATCGGAGAGATAGAGAAATATGAGAGTGGTGGTGGAGAACAA 443
Db 392 tactactgtagtagaatccggaagatagaggatattgaaagtggtggggaaccaaaaa 451
QY 444 TCTCTCACTGAAAGAGCAAGCAACTGGGGAGATAGTGAGCCCAACAAACAGAGAACAG 503
|||||
Db 452 tctcttactgaagaagcaggaactcgggagatggtgagcccaacaagaagaacaag 511
QY 504 GAGGACTGCGTGAGATCTATATCAAGAGAAACAAAGATGCAAGCAAAATGGAAGATGAC 563
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Db 512 gaggaactcgttgagatctatatacaagaagaacagatgcaggaacaaatggaacgtag 571
QY 564 GCGTGCACAAACTTAAAGCAGCCCTCTGTACACAGCTTCTTGCCAGCCCTGGTCAATGC 623
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Db 572 gctgcacaacaactaaagcagccctctgttaacacagcttctgcagccctgctatgc 631
QY 624 AGTGGCATGGAGAGATGTGTAAGAAATCATCAATATACACACTGCAACTGTATGTGGG 683
|||||
Db 632 agtggccatggaagaaatgctgagaatacatcaataatcacctgcaactgtagtggg 691
QY 684 TACTATGGGCCCAAGTGTGAGCTTGTGATTCAGTGTGAGCTTGGAGGCCCAAGGCTG 743
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Db 692 tactatggcccaagtgctgaatttgatctcagtgtagaccccttgaggcccaagagctg 751
QY 744 GGTACCATGACGTGTACTACCCCTTGTGAAACTTACGCTTACGCTCACAGTGTGCTTC 803
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Db 752 ggtacacatgactgtactaccccttgaggaaacttcagcttcacagctgtagcttc 811
QY 804 AGTGTGCTGAGAGAACTTAACGCGGATGTGAGAAACCAACCTGTGACCATTTTGA 863
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Db 812 agctgtctgaaagaaacaaacttaactcggatctgaaagaacacacccgtgtagcatttga 871
QY 864 AACTGTGATCTTCAGAACCCACTGTCAGTGTGATTCAGTGTGAGGCTGTATGACGACCA 923
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Db 872 aactgtctatctccagaaacaaactgcaagatctcagtgtagagctctctatcagaacca 931
QY 924 GATTTGGGATCATGAACTGTAGCCATCCCTGGCCAGCTTACGCTTACCTGTGCATGT 983
|||||
Db 932 gatcttggaatcatgaaactgttagccatccctggccagcttcacttacctctgcatgt 991
QY 984 ACCTTATGCTGCAGAAAGAACTGATTAATTGGGAGAGAAACCACTTTGTGATTA 1043
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Db 992 accttcatctgctcgaagaagaaactggttaatttgggaagaagaacacatcttgaatca 1051
QY 1044 TCTGGAATCTGTCAAAATCTAGTCCAAATATGTCAAAAATTGCAAAAAGTTTCAATG 1103
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Db 1052 tctggaatctgttcaaatcttagtccaataatgcaaaaattgagcaaaaagttctcatg 1111
QY 1104 ATTAAAGAGAGGATTTATTAACCCCTCTTCAATTCAGTGTGACGTCATGTTACTGCATTC 1163
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Db 1112 attaaagaggtgattataacccctcttcatctcagtgtagcagtcattgltactgcatlc 1171
QY 1164 TCTGGGTTGGCATTTATCATTTGGCTGGCAAGAGATTAAAAAGCAAGAAATCCAAAG 1223
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Db 1172 tctgggttggaatttatacatcttgcttgcgaaggaattcaaaaaggaagaaaccaaag 1231
QY 1224 AGAAGTATGAATGACCCATTTAAATTCGCCCTTGTGTAAGAAATTTCTTGAATATCTAA 1283
Db 1232 agaagtatgaatgaccatattaaatcgcccttggtagaagaanaattcttgaaataactaa 1291
QY 1284 AATATGATGATTCCTTTAAATCCTTCCATGAACGCTTTTGTGTGTGGCACCTCCTTACGT 1343

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Db 1292 aaatcaatgagatccctttaaatcccttccatgaaacgttttgggtggccacctcaagt 1351
QY 1344 CAACATGAGAGTGTG-TTCCCTGATGTCATCTGGGAAAGATTCTTACCCACCAAGCTTC 1402
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Db 1352 caaaatgaaagtgtgttcccttcaagtcagcctcgggaagattcttaccatgacaacagctc 1411
QY 1403 CTTCAGCTTCCATTTGCGCCCTCATTTATTCCTCAACCCCCAGCCCAAGGTTTATAC 1462
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Db 1412 cttaagcttccatttgcgccctcatattatccctcaacccccccagcccaagtggttatcc 1471
QY 1463 AGCTACACTTTTGTCTTTCTGTGAGAGAAACAAATTAAGCAAT- AAGGAAAGATTCA 1521
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Db 1472 agcccaacttcttgcttcttctgaaggaaacaaataaagacataaaggaaagattca 1531
QY 1522 TGTGATATTAAGATAGGCTGACTTGTGCTCTTCTTGTGACTTGTGTTTGTAGTTCAATTG 1581
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Db 1532 tgtggaatataaagatgagcgtgacttgccttcttctgactcttglttcaagttcaatlc 1591
QY 1582 AGTGTGTACTTGTATGACAGACACTTCTTAATGAAGTGCAAATTTGATATATGTGAT 1641
|||||
Db 1592 agtgcgtacttgatgacagacacttcaatgaaatgcaaatgtgatacatatgtgat 1651
QY 1642 ATGACATCACTTTCTTGGAGATCAAAATTTCAAGCTGCTGTCTGTATACTGTGAGTAC 1701
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Db 1652 atggaactcagtttcttgcagatcaaatcttcaagctgtcttctgtatatacttgvgaagta 1711
QY 1702 ACTCTTATGAAAGATTCAAAAGTGTACGCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1761
|||||
Db 1712 actcttatagaagaatgtaaaagcttcaagcttcttcttcttcttcttcttcttcttcttct 1771
QY 1762 TGGGCTCTGCTCAAGTTTAAAGAGTCCATTTGTGACGTGTAGCTGCGCTGTGAAAT 1821
|||||
Db 1772 tggggtcctgctcaagttgaaagagcttcaatgtgacgttagccctgcgcgtctgaaat 1831
QY 1822 GGACCATCTTATTTAACTGAGCTTCAAGGCTCCCGACCTTCTTCAAGCCACCTCTTTTC 1881
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Db 1832 ggaacatctatatttaacggtctca-gcttcccaacttctcagccaactcttcttct 1890
QY 1882 AGTGGCTGTACTTCCACACACTATGATCATGATGATGCCAAAGAGAGAGAGAGA 1941
|||||
Db 1891 agtggctgacttccacacacttagcatctcagtggtgccaagcaaaaggaggaagaga 1950
QY 1942 AATAGCGTGGCGGTTTTTTAGTTGGGGTTTTGCTGTCTTTTATGAGACCCATTC 2001
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Db 1951 aatagcctggcgtcttctttagtgggtgttgcgtgttcccttattagagaccatc 2010
QY 2002 CTATTTCTTATAGTCAATGTTCTTTTATACGATATTATATGTAAGAAACATCACTGA 2061
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Db 2011 ctatttctataagtaaatgttcttcttcttcaacgatatattatagaaagaacacacactga 2070
QY 2062 AATGTACTGCAAGTGCATCTCTTTGATGTCAATGAAAGACTTAAACAGGTGAGAGA 2121
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Db 2071 aatgtactgtcgaagtgcacatctcttgaatgtcatatggaagagttaaacaggtgaga 2130
QY 2122 AATTCCTGATTCAAAATGAAATGCTCTCTTCCCTTCCCTGCCCCAGAACTTTATGCAC 2181
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Db 2131 aatcccttgatcccaatgaaatgctccttcccttccctgcccccaagaaactttatccact 2190
QY 2182 TACCTAGATTCTACATATCTTTAAATTTCAATTCAGAGGCTCCCTCAACCCCA 2235
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Db 2191 tacttagattctataatcttcttaaatcttcaatctcaggtccctccctcaaccac 2244

RESULT 8
US-60-172-373-15742
; Sequence 15742, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequences, and Single Nucleotide Polym

FILE REFERENCE: GX-0006.P
CURRENT APPLICATION NUMBER: US/60/172.373
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 25,772
SOFTWARE: PERL Program
SEQ ID NO 15742
LENGTH: 2387
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 331616.2
US-60-172-373-15742

Query Match 94.3% Score 2129.6; DB 49; Length 2387;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2201; Conservative 0; Mismatches 9; Indels 6; Gaps 6;
QY 25 ACCTGACGACACA-GCACACTCCCTTT-GGCAAGACCTGAGACCCCTGTGCTAGT-CAA 81
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32 accctgcagcacaagcacactccctcttgycagaagacctgagacctctgtctaaagtcaca 91
QY 82 GAGGCTCAATGGGCTGCGAGAAGACTAGAGAAGACCAAGCAAGCCATGATTTTCAT 141
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
92 gaggtcacaatggtgctgcagaagaactagagaagaccaaagcaagccatgatatctccat 151
QY 142 GAAATGTCAAGACCAACCAGAGGACTTATGAAACATCTTCAAGTTGTGGGGTGGACAA 201
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
152 ggaattctcagagaccaccagaggaactatgaaacatctccaagtcttg9999tgcgacaa 211
QY 202 TGCCTCTTGTGATTTCTCTGGACATCATGGAACCTACTGCTGACTTACCATTTATCTG 261
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
212 tgcctctctgaltcttcctgcgcacatcatctgaaccgactctgactaccatattctcg 271
QY 262 AAAAACCATGAACTGGCAAAAGGCTAGAAAGATTCTGCCGAGCAATTAACAGATTAG 321
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
272 aaaaaccatagaactcgcagaaggtctagaagatctctgcgagaataataacagatttag 331
QY 322 TTGGCATACAAAACAGCGGAAATTGATATCTGAGAAGACTCTGCCCTTCAGTCTG 381
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
332 ttgcatacaaaaacaagcggaattgactatctgagaagactctgccttcagtcgtt 391
QY 382 CTTAATCTGATGATGAAATCCGAAATAGAGAAATATGAGACTGGGTGGGAACCAACA 441
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
392 cttaactctggaataagatcccgagaataagaaataatgaaagcttg9999aaaccaca 451
QY 442 AATCTCAGTGAAGAGACAGAGAACTGGGAGATGGTGAGCCCAACAACAGAAGACA 501
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452 aatctcactatgaagaagacgagaactcgg9999agatggtgcgccaacaacaagaagaca 511
QY 502 AGGAGACTCGTGAGAGATCTATATCAAGAAACAAAGATGACGGCAATGGAACGATG 561
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512 ag9999actcgtg9999actatatacaagaagaacaaagatgcagcaaatg9999gatg 571
QY 562 ACGCTGCCCCAACAACCTAAAGGACGCCCTCTGTACACAGCTTCTGGCAGCCCTGGCAT 621
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
572 acgcctgcacaacaactaaagcagccctctgttaccagactctcttgccaagccctgcat 631
QY 622 GCAATGGCATGAGAACTGTAGAAATCAATCAATCAACACTGCAACCTGATGTGG 681
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
632 gcaatggtcactgagaaatctgtagaataatcaataataataactgcaactgt9999tgg 691
QY 682 GGTACTATGAGGCCCACTGCTAGCTTGATTCAGTGTGAGCCCTTGGAGGCCCCAGAGC 741
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
692 gttactatg9999cccaagtgtcagtttgatctcagttg9999ccttg9999cccaagc 751
QY 742 TTGGTACCATGAGACTGATACACCCCTTTGGAAACTCAGCTTACGCTACAGTGTGCT 801
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
752 ttgggtacacatgagactgactaacctcttg9999aaactcagctcagctcag9999cct 811
QY 802 TCAGCTCTCTGAAGAAACAACCTTAAGTGGATTGAAGAAACCACTGTGACCAATTTG 861
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

DB 812 tcagctgctcgaaggaagacaacttaactggtatgaaagaacccaacctgtgagaccattg 871
QY 862 GAAACTGCTCATCTCCAGAACCAACCTGTCAAGTGAATTCAGTGTGAGGCTCTATCAGCAC 921
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
872 gaaactgtcatctcccaagaacaacctgtcaagtgatctcagtggtgagctctatcaagcac 931
QY 922 CAGATTTGGGGATCATGAACTGATGCCATGCCCGGCCAGCTTCAGCTTACCTGTGCAT 981
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932 cagatttgg9999atcaatgaactcgtagccaatccccg9999cagctccaagcttaccctcgat 991
QY 982 GTACCTTCATCTGCTCAGAAAGAACTGAGTTAATTTGGAAAGAAACCAATTTGTGAAAT 1041
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
992 gtaccttcattctgctcagaagaaactgagttaattg9999aagaagaaacacattgtgacat 1051
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1052 catctggaatctggtccaatccctagtcacaatgtccaanaaattg9999aagattctcaca 1111
QY 1102 TGATTAAGGAGGATGATTAATTAACCCCTTCATTTCCAGTGGCAGTCAATGGTTACTGCAT 1161
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1112 tgattaa9999agatataaaccctctcatctcagtg9999atcaatg9999tactgcat 1171
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1172 tctctggttggcatcttcatctctgctgcagaagagatcaaaaaaagcgcaagaatcca 1231
QY 1222 AGAGAAGTGAATGACCCATATTAAATCGCCCTTGTTGTAAGAAATTTCTTGAATACT 1281
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1232 agagaagatgaatgagaccatataaatacgcctctgtg9999aagaanaattcttg9999tact 1291
QY 1282 AAAATCATGATGATCCTTTAAATCCTTCAGTAAGAAACGTTTGTGGGAGACCTCCAC 1341
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1292 aaaaatcatgagatccctttaaataccttccatcg9999aagcttg9999gagacccctcac 1351
QY 1342 GTCAACATGAAAGTGTG-TTCTCTCAGTGCATCTGGGAGAGATTCTCCAGCCAGCAACAGT 1400
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1352 gtcaaatatgagatggtgttctctcagtgatctcgg9999aagttcttcaactgacaaagct 1411
QY 1401 TCTTTACGCTTCATTTTGCCCTTCATTTATCCTCAACCCCAAGCCCAAGGTGTTAT 1460
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1412 tctctcagctcccatctcgcgcccatattacccccaaccccgccaagctgattcat 1471
QY 1461 ACAGCTCAGCTTTTGTCTTTCTTGAGGAGAAACAATTAACAGCAT-AAGGAAAGAGTT 1519
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1472 acagctcagctctctctctctcgc9999aagaacaaaataacacataag9999aagatt 1531
QY 1520 CATGTGAAATATAAGATGAGCTGACTTGTGCTTCTTGAATCTTGTGATTCAT 1579
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1532 catgtgaaataataaagatggtgactcttctcttctgactctgttctcagtttccat 1591
QY 1580 TCACTGCTGTAAGTGAAGACAGACACTTCTTAATGAAGTGAATTTGATNCAATGTGA 1639
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1592 tcaagtgcactatgagacagacactctaaagagtg9999aatttgatatacatgtga 1651
QY 1640 ATATGAGACTCAGTTTCTCTGAGATCAAAATTTACAGTCGTCTCTGATACTGTGGAGGT 1699
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1652 atatgagactcagttctctcgcagatacaaatctcagctcgtctctgtatatactg9999gt 1711
QY 1700 ACACCTTATAGAAAGTTCAAAAAGTGTACGCTCTCTCTTCTTCTTAATCTCAGTGAAGT 1759
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1712 acactcttatagaaagttcaaaaaagttcagctctctctcttcttcaactcagtg9999gt 1771
QY 1760 AATGGGCTCTGCTCAAGTTGAAAGAGTCTATTGCACTGTAGCCCTGCGCTGTGTGA 1819
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1772 aatggggtctcgtccaagtgtgaagagttcattatgcaactgagcctcgcgtctgtga 1831
QY 1820 TTGGACCATCCTATTTAACGTGGCTTCAGGCTCTCCCAACCTTCTTCAAGCAACCTCTCTTT 1879
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1832 ttggacatctctatcttaactggtctca-gcctcccaactcttcaagccacactctctctt 1890
QY 1880 TCAGTTGGCTGACTTCCACACACTAGATCTCATAGTGGCCAAAGCAAGAGAGAGAGA 1939
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1891 tcaagtgtgacttccacaactctgactctcatgagtg9999aagaag9999aag9999a 1950

QY	1940	GAATAGCGTCGCGGGTGTGTTTGTGTTGGGGGTTTGCGTTCCTTTATGAGACCCAT	1999
Db	1951	gaatagcctgcgcgtctgttttttagtttgcgttggtgggttttgcgttctttaaagaccat	2010
QY	2000	TCTATTTCCTTAATAGTCAATGTTTCCTTTATGACGATATATTAGTAAGAAACATCACT	2059
Db	2011	tcctatttcttaatagtaacaaagtcttcttttaacagatatattagtaagaacaatcaact	2070
QY	2060	GAATTCGTACTCTGCAAGTGCATCTCTTTGATGTGATATAGTAAGAGTATAAACAAGTGGGA	2119
Db	2071	gaatgcctagctgcgaagtagcaccctctttagatcatatagaagaagtttaaaacagtg19ga	2130
QY	2120	GAATTCCTTGATTCACAATGAATGAAATGCTCTCCCTTCCCTGGCCCCAGACATTTTATCA	2179
Db	2131	gaatttccttgattcacaagaatgctctccttctcccttccctgcgcccgagaactttatcca	2190
QY	2180	CTTACCGTCAGATTTACATATTTCTTTAAATTTATGATCGAGCCTCCCTCAACCCAC	2235
Db	2191	cttaaccagatctacatatatctttaaacttcatcttcagtcgctccctccctaaccaccac	2246

RESULT 9
 PCT-US92-03970-1
 Sequence 1, Application PC/TUS9203970
 GENERAL INFORMATION:
 APPLICANT: Dana-Faber Cancer Institute, Inc.
 TITLE OF INVENTION: LEUKOCYTE-ASSOCIATED CELL SURFACE
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
 STREET: Ten Post Office Square
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/03970
 FILING DATE: 19920513
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Heine, Holliday C.
 REGISTRATION NUMBER: 34,346
 REFERENCE/DOCKET NUMBER: DFCI-152Bq9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-2290
 TELEFAX: (617) 451-0313
 TELEX: 940675
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2330 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEetical: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 53..1210
 PUBLICATION INFORMATION:
 DOCUMENT NUMBER: US 07/700,773
 FILING DATE: 15-MAY-1991
 PCT-US92-03970-1

Best Local Similarity 98.5%; Pred. No. 0;
Matches 2161; Conservative 0; Mismatches 24; Indels 9; Gaps 5

QY	44	CGTTTGGGAAAGAGACCTTGAGACCTTGTGCTTAAGTCAAGAGAGCTCAATAGAGGCTGCACAAAG	104
Db	7	CCCTTTGGGGCAAGAGACCTTAGAGACCCCTTTGTGCTTAAGTCAAGAGAGGCTCAATAGGGCTGCAGAAAG	66
QY	104	AACTAGAGAGAGACCAAGCAAAAGCCATATATTTTTCATGTGAAATGTGAGAGACCCACAGAG	163
Db	67	AACTAGAGAGAGACCAAGCAAAAGCCATATATTTTTCATGTGAAATGTGAGAGACCCACAGAG	126
QY	164	GGACTTATGGAACATCTTCAAGTGTGTGGGGGTGACACAATGCTGTGTGTATTTCTGTGG	223
Db	127	GGACTTATGGAACATCTTCAAGTGTGTGGGGGTGACACAATGCTGTGTGTATTTCTGTGG	186
QY	224	ACATATGGAACCTACCTGCTGGACTTACCATTTTCTGAAAAAACCCATGAACTGGCAAAAG	283
Db	187	ACATATGGAACCCGACTGCTGGACTTACCATTTTCTGAAAAAACCCATGAACTGGCAAAAG	246
QY	284	GGCTAGAGATTCTGCCGAGACAATTAACACAGATTATGTTGGCATACAAACAAAGCCGGA	343
Db	247	GGCTAGAGATTCTGCCGAGACAATTAACACAGATTATGTTGGCATACAAACAAAGCCGGA	306
QY	344	AATTGAGTATCTGGAGAAAGACTGTCGCTTACGTGTTTCTTACTGATAGAAATCCG	403
Db	307	AATTGAGTATCTGGAGAAAGACTGTCGCTTACGTGTTTCTTACTGATAGAAATCCG	366
QY	404	GAAGATAGSAGAAATATGAGACGTGGGTGGGAGACCAACAATCTCTACAGTAAGAAACACA	463
Db	367	GAAGATAGSAGAAATATGAGACGTGGGTGGGAGACCAACAATCTCTACAGTAAGAAACACA	426
QY	464	GAAGTGGGGAGATGGTGAAGCCCAACAAGAAAGAACAAAGAGAGACTGGGTGAGATCTA	523
Db	427	GAAGTGGGGAGATGGTGAAGCCCAACAAGAAAGAACAAAGAGAGACTGGGTGAGATCTA	486
QY	524	TATCAAGAGAAACAAGATGAGGCCAATATGAAAGATGAGACGCTGCCACAAACTAAAGGC	583
Db	487	TATCAAGAGAAACAAGATGAGGCCAATATGAAAGATGAGACGCTGCCACAAACTAAAGGC	546
QY	584	AGCCCTGTTTACACAGCTTCTTCCAGCCCTGGTATGATGAGTGGGCATGAGAAATGTGT	643
Db	547	AGCCCTGTTTACACAGCTTCTTCCAGCCCTGGTATGATGAGTGGGCATGAGAAATGTGT	606
QY	644	AGAAATATCATATATACACACCTGSCAACTGTATGTGGGTACTATAGGCCCCAGTGTCA	703
Db	607	AGAAATATCATATATATACACACCTGSCAACTGTATGTGGGTACTATAGGCCCCAGTGTCA	666
QY	704	GCTGTGATTAAGTGAAGCCTTTGGAGGCCGACAGAGCTGGGTACCATGAGACTGTACTCA	763
Db	667	GTTTGTGATTTAGTGTGAGCCTTTGGAGGCCGACAGAGCTGGGTACCATGAGACTGTACTCA	726
QY	764	CCCTTTTGGAAACTTTCAGCTTCAGCTTCACAGTGTGCTTTCAGCTGCTGGAAGGAACAA	823
Db	727	CCCTTTTGGAAACTTTCAGCTTCACAGTGTGCTTTCAGCTGCTGGAAGGAACAA	786
QY	824	CTTAACCTGGGATTAAGAAACCAACCTGTGACCATTTGAAACTGGTCAATCTCCAGAAC	883
Db	787	CTTAACCTGGGATTAAGAAACCAACCTGTGACCATTTGAAACTGGTCAATCTCCAGAAC	846
QY	884	AAACCTGCAAGTGAATTCAGTGTGAGCCTTATACAGACCAAGATTTGGGGATCATCAACTG	943
Db	847	AAACCTGCAAGTGAATTCAGTGTGAGCCTTATACAGACCAAGATTTGGGGATCATCAACTG	906
QY	944	TAGCAGCATCCCTGGCCAGCTTTCAGCTTTACCTGTGATGTACCTTCATATCTGTCAAGAG	1003
Db	907	TAGCAGCATCCCTGGCCAGCTTTCAGCTTTACCTGTGATGTACCTTCATATCTGTGTCAAGAG	966
QY	1004	AACAGCATTAATTGGGAAAGAAAGAAACCAATTTGTGAATATCTGGAAATCTGGTCAAAATCC	1063
Db	967	AACAGCATTAATTGGGAAAGAAAGAAACCAATTTGTGAATATCTGGAAATCTGGTCAAAATCC	1026
QY	1064	TAGTCATATATGTCAAAAATTTGACAAAAGTTTCTCAATGATTAAGAGAGGTGATTATTA	1123

Db 1027 TAGTCCAAATATGTCAAAAATTGGACAAAGTTTCTCATGATTAAGGAGGTGATTTAA 1086
QY 1124 CCCCCTTCATTCACAGTGGCACTCATGTTACTGATTCCTGGGTTGGCAATTTATCAT 1183
Db 1087 CCCCCTTCATTCACAGTGGCACTCATGTTACTGATTCCTGGGTTGGCAATTTATCAT 1146
QY 1184 TTGGCTGGGCAAGAGATTAAGGCAAGAAATCCAAAGAAAGTGTGAAATGACCCATA 1243
Db 1147 TTGGCTGGGCAAGAGATTAAGGCAAGAAATCCAAAGAAAGTGTGAAATGACCCATA 1206
QY 1244 TTAAATCGCCCTTGTAAGAAATTTCTGAATACTAAATAATCATGATCCTTTAAA 1303
Db 1207 TTAAATCGCCCTTGTAAGAAATTTCTGAATACTAAATAATCATGATCCTTTAAA 1266
QY 1304 TCCCTTCAGTAAACGTTTGTGTGGTGACCTTCCTACGTCAAACATGAAGTGTG-TTCC 1362
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QY 1363 TTGAGTGCATCTGGGAAGATTTCTACCCGACCAAGTTCCCTTCAGTTCATTTGCCCC 1422
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QY 1423 CTCATTTATCCTCAACCCCGACCCACAGGTGTTATACAGCTCAGCTTTTGTCTTT 1482
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QY 1542 GACTTGGCTCTTCTGACCTCTGTTTTCAGTTTCAATAGAGTGGTACTTATATGACAG 1601
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QY 1602 ACACCTTAATGAAGTGAATTTGATACATATGTGAATAGTACACTTTTCTTGCA 1661
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QY 1662 GATCAAAATTTACAGTGTCTTGTGTATACTGTGGAGTACACTCTTAATGAAGTTCAA 1721
Db 1627 GATCAAAATTTACAGTGTCTTGTGTATAC-GTGGAGGTACACTCT----ATGAAGTCAA 1680
QY 1722 AAGTCAAGCTCTCTCTTCTTCTTAACCTCAGTGAAGTAAATGGGTCCTCTCAAGTGA 1781
Db 1681 AAGTCAAGCTCTCTCTTCTTCTTAACCTCAGTGAAGTAAATGGGTCCTCTCAAGTGA 1740
QY 1782 AAGAGTCTATTTGCACTGAGCTGCGCTGTGTGAATGAGCAATCTAATTTAACTGG 1841
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QY 1842 CTTGAGGCTCTCCCACTCTCTTTCAGCCACCTCTTTTTCAGTTGGCTGACTTCACACC 1901
Db 1801 CTTGCA-GCCGCCCCCACTCTCTTTCAGCCACCTCTTTTTCAGTTGGCTGACTTCACACC 1859
QY 1902 TACGATCTCATGAGTGGCAAGCAAAAGAGAGAGAGAAATAGCTGGCGGTTTTTT 1961
Db 1860 TACGATCTCATGAGTGGCAAGCAAAAGAGAGAGAGAAATAGCTGGCGGTTTTTT 1919
QY 1962 AGTTTGGGGTTTTGCTGTTTTCTTTATGAGACCATTCCTAATTTCTTAATGCAATGT 2021
Db 1920 AGTTTGGGGTTTTGCTGTTTTCTTTATGAGACCATTCCTAATTTCTTAATGCAATGT 1979
QY 2022 TTCTTTTATCAGATATTAATTAAGAAACATCACTGAATGCTAAGCTGCAAGTGACA 2081
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PCT-US94-00909-1
? Sequence 1, Application PC/TUS9400909
? GENERAL INFORMATION:
? APPLICANT:
? TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS BLOCKING
? TITLE OF INVENTION: AGENTS FOR COMPONENT SELECTIN FUNCTION
? NUMBER OF SEQUENCES: 11
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT/US94/00909
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/008,459
? FILING DATE: 25-JAN-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/983,606
? FILING DATE: 30-NOV-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/962,483
? FILING DATE: 02-APR-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/770,608
? FILING DATE: 03-OCT-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/737,092
? FILING DATE: 29-JUL-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/730,503
? FILING DATE: 08-JUL-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/700,773
? FILING DATE: 15-MAY-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/313,109
? FILING DATE: 21-FEB-1989
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2330 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 53..1210
? PCT-US94-00909-1
Query Match 92.4%; Score 2087.6; DB 1; Length 2330;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2161; Conservative 0; Mismatches 24; Indels 9; Gaps 5;
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Db 7 CCGTTGGCAAGGACCTGAGACCTTGCTAAGTCAAGAGGCTCAATGGGCTGCAGAG 66
QY 104 AACTAGAGAGGACCAAGCAAGCATGATTTTCCATGGAATGTCAAGACCCAGAG 163
Db 67 AACTAGAGAGGACCAAGCAAGCATGATTTTCCATGGAATGTCAAGACCCAGAG 126
QY 164 GGAATTATGGAACATCTTCAAGATTGTGGGGGTGGAACAATGCTCTGTGTTGATTTCCCTGGC 223

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Db 127 GGACTTATGAAACATCTTCAAGTTGTGGGGGTGAGCAATGCTCTGTGTGATTTCTTGCC 186
QY 224 ACATATGAGAACTTCTGCTGTGACTTACCATTATTTCTGAAAAAACCATTGAATGCGCAAG 283
Db 187 ACATATGAGAACTTCTGCTGTGACTTACCATTATTTCTGAAAAAACCATTGAATGCGCAAG 246
QY 284 GGCCTGAGAACTTCTGCTGTGACTTACCATTATTTCTGAAAAAACCATTGAATGCGCGGA 343
Db 247 GGCCTGAGAACTTCTGCTGTGACTTACCATTATTTCTGAAAAAACCATTGAATGCGCGGA 306
QY 344 AATTGAGTATCTGAGAACTTGTGCTTCAAGTCTTCTTACTACTAGATAGGAATCCG 403
Db 307 AATTGAGTATCTGAGAACTTGTGCTTCAAGTCTTCTTACTACTAGATAGGAATCCG 366
QY 404 GAAATGAGAGAAATATGAGAACTGCTGGTGGGAAACCAACAATCTCTCACTGAGAAAGAGA 463
Db 367 GAAATGAGAGAAATATGAGAACTGCTGGTGGGAAACCAACAATCTCTCACTGAGAAAGAGA 426
QY 464 GAACCTGGAGAGATGAGAGCCCAACAACAAGAGAGAGAGAGAGAGAGAGAGATCTA 523
Db 427 GAACCTGGAGAGATGAGAGCCCAACAACAAGAGAGAGAGAGAGAGAGAGATCTA 486
QY 524 TATCAAGAGAAACAAGATGAGCAAAATGGAACGATGAGCCCTGCCAACAATGAAAGC 583
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QY 584 AGCCCTGTATACAGACTTCTTCCAGCCCTGTGCTATGAGAGAGAGAGAGAGAGATGT 643
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QY 644 AGAATCATCAATATACACACCTGCAACTGTGATGAGGGGTACTATGAGCCCGCAAGTCA 703
Db 607 AGAATCATCAATATATACACCTGCAACTGTGATGAGGGGTACTATGAGGGCCCAAGTCA 666
QY 704 GCTTGTATCAAGTATGAGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCTCA 763
Db 667 GCTTGTATCAAGTATGAGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCTCA 726
QY 764 CCCCCTTGGAACTTCAAGTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 823
Db 727 CCCCCTTGGAACTTCAAGTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 786
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QY 884 AACCTGTCAAGTATGAGTGAAGCTGATGAGCAAGAGAGAGAGAGAGAGAGAGAGAG 943
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Db 1027 TAGTCCATATGCAAAATGAGCAAAAGTTTCTCAATGATTAAGAGAGAGAGAGATTA 1086
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QY 1244 TTAATCGCCCTTGTGAG 1303
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Db 1207 TTAATCGCCCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1266
QY 1304 TCCCTTCATGAAAGCTTTGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1362
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QY 1363 TTGAGTCAATCTGGAGAGAGATTTTACCCGACCAAGAGAGAGAGAGAGAGAGAGAG 1422
Db 1327 TTGAGTCAATCTGGAGAGAGATTTTACCCGACCAAGAGAGAGAGAGAGAGAGAG 1386
QY 1423 CTCATTTATCCCTCAACCCCGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1482
Db 1387 CTCATTTATCCCTCAACCCCGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1446
QY 1483 CTGAG 1541
Db 1447 CTGAG 1506
QY 1542 GACTTTGCTCTTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1601
Db 1507 GACTTTGCTCTTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1566
QY 1602 ACACCTCTTAAATGAG 1661
Db 1567 ACACCTCTTAAATGAG 1626
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QY 1722 AAGTGTAGCTGCTGCTTCTTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1781
Db 1681 AAGTGTAGCTGCTGCTTCTTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
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Db 1741 AAGAGTCTTATTTGAG 1800
QY 1842 CTTTACGAGCTTCCCACTTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1901
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QY 2022 TTCTTTTATCAGATATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2081
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QY 2082 TCTCTTGTATGATATGAG 2141
Db 2040 TCTCTTGTATGATATGAG 2099
QY 2142 AATGCTCTCTTCTTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2201
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QY 2202 TTTAAATTTTCACTCAG 2235
Db 2160 TTTAAATTTTCACTCAG 2193
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RESULT 11
US-08-008-459-1
; Sequence 1, Application US/08008459
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; APPLICANT: Kansas, Geoffrey S.

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QY	1304	TCCTTCATGAAGCGTTTGTGTGGTGGACCTCCTACGTCCAAACATGAAGTGTG - TTCC	1362
Db	1267	TCCTTCATGAAGCGTTTGTGTGGTGGACCTCCTACGTCCAAACATGAAGTGTGTTC	1326
QY	1363	TTGAGTGCATCTGGGAAGATTTCTACCCGACCAACAGTTCCTTAGCTTCATTTCGGCC	1422
Db	1327	TTGAGTGCATCTGGGAAGATTTCTACCTGCACCAACAGTTCCTTAGCTTCATTTCACCC	1386
QY	1423	CTCATTTATCCCTCAACCCCGACGCCACAGTGTATTACAGCTCAGCTTTTGTCTTTT	1482
Db	1387	CTCATTTATCCCTCAACCCCGACGCCACAGTGTATTACAGCTCAGCTTTTGTCTTTT	1446
QY	1483	CTGAGGAGAAACAATTAAGACCAT - AAGGAGAAAGATTCATTGTGAAATATAAAGATGGCT	1541
Db	1447	CTGAGGAGAAACAATTAAGACCATATAAGGAGAAAGATTCATTGTGAAATATAAAGATGGCT	1506
QY	1542	GACCTTCCTCTTCCTGACCTGTGTTTCACTTCATTCAGTCTCTACTGTATGACAG	1601
Db	1507	GACCTTCCTCTTCCTGACCTGTGTTTCACTTCATTCAGTCTCTACTGTATGACAG	1566
QY	1602	ACACTTCCTAAATGAAGTGCAAAATTTGATACATATATGTAATGAGACACAGTTTCTTCGA	1661
Db	1567	ACACTTCCTAAATGAAGTGCAAAATTTGATACATATATGTAATGAGACACAGTTTCTTCGA	1626
QY	1662	GATCAAAATTCACAGTGTCTCTTGATATCTGTGAGGTACACACTTATAGAAAGTTCAAA	1721
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QY	1722	AAGTCTACGCTCTCCTTTCTTTCTAACTCCAGTAAGATATGGGTCCTGCTCAAGTTGA	1781
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QY	1782	AAGATTCCTATTGCACTGTAGCGTCGCGCTGTGTAATTGGAACATCCTATTAACTGG	1841
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QY	1842	CTTCAGAGCCCTCCGACCTCTCTAGACACCTCTCTTTTATGTTGGCTGACTCCACACC	1901
Db	1801	CTTCA - GCCCTCCGACCTCTCTAGACACCTCTCTTTTATGTTGGCTGACTCCACACC	1859
QY	1902	TAGCATCTCATGATGCCAAGCAAGCAAGAGAGAGAGAAATATAGCTGCGCGTTTT	1961
Db	1860	TAGCATCTCATGATGCCAAGCAAGCAAGAGAGAGAGAAATATAGCTGCGCGTTTT	1919
QY	1962	AGTTTGGGGGTTTGTCTGTTTCTTTTATGAGACCAATTCATTTTCTTATAGTCAATGT	2021
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QY	2022	TTCTTTTATCAGATATTTATTTAGTAGAAACAATCCTGAAATGCTAGCTGCAAGTACA	2081
Db	1980	TTCTTTTATCAGATATTTATTTAGTAGAAACAATCCTGAAATGCTAGCTGCAAGTACA	2039
QY	2082	TCCTTTTATGTCATATGAGAGAAGTTAAACAAGTGTGAGAAATCTCTTATTCACATGA	2141
Db	2040	TCCTTTTATGTCATATGAGAGAAGTTAAACAAGTGTGAGAAATCTCTTATTCACATGA	2099
QY	2142	AATGCTCTCTTTCCCTCGCCCGACAGACTTTTATCCACTTACCTAGATTCACATATTC	2201
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US-08-340-539-1
; Sequence 1, Application US/08340539

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1  GENERAL INFORMATION:
2  APPLICANT: Tedder, Thomas F.
3  APPLICANT: Kansas, Geoffrey S.
4  TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
5  TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
6  NUMBER OF SEQUENCES: 11
7  CORRESPONDENCE ADDRESSES:
8  ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
9  STREET: Ten Post Office Square
10 City: Boston
11 STATE: MA
12 COUNTRY: USA
13 ZIP: 02109
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/340,539
22 FILING DATE: 16-NOV-1994
23 CLASSIFICATION: 514
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 08/008,459
26 FILING DATE: 25-JAN-1993
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 07/993,606
29 FILING DATE: 30-NOV-1992
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 07/862,483
32 FILING DATE: 02-APR-1992
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: US 07/770,608
35 FILING DATE: 03-OCT-1991
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: US 07/737,092
38 FILING DATE: 29-JUL-1991
39 PRIOR APPLICATION DATA:
40 APPLICATION NUMBER: US 07/730,503
41 FILING DATE: 08-JUL-1991
42 PRIOR APPLICATION DATA:
43 APPLICATION NUMBER: US 07/700,773
44 FILING DATE: 15-MAY-1991
45 PRIOR APPLICATION DATA:
46 APPLICATION NUMBER: US 07/313,109
47 FILING DATE: 21-FEB-1989
48 ATTORNEY/AGENT INFORMATION:
49 NAME: Heine, Holliday C.
50 REGISTRATION NUMBER: 34,346
51 REFERENCE/DOCKET NUMBER: DDCI-318XX
52 TELECOMMUNICATION INFORMATION:
53 TELEPHONE: (617) 542-2290
54 TELEFAX: (617) 451-0313
55 TELEX: 940675
56
57 INFORMATION FOR SEQ ID NO. 1:
58 SEQUENCE CHARACTERISTICS:
59 LENGTH: 2330 base pairs
60 TYPE: nucleic acid
61 STRANDEDNESS: single
62 TOPOLOGY: linear
63 MOLECULE TYPE: cDNA
64 HYPOTHEICAL: NO
65 ANTI-SENSE: NO
66 FEATURE:
67 NAME/KEY: CDS
68 LOCATION: 53..1210
69 PUBLICATION INFORMATION:
70 DOCUMENT NUMBER: US 07/700,773
71 FILING DATE: 15-MAY-1991
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73 US-08-340-539-1

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Query Match 92.4%; Score 2087.6; DB 7; Length 2330;

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Db 372 aactacgtgataggaaatccggaagaatagagaataatagaaagtgggagggaaccaaat 421
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Db 492 aggaactgctgagagatctataatcaagaagaacaagatgcaaggcaaatggaacgatacg 551
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Db 792 gctgctctgaagaaacaaacttaacgtggaatgaagaacacactgtgagccattgga 851
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QY 1464 GCTCAGCTTTTGTCTTTCTGTGAGAGAAACAATTAAGACCTT-AAAGGAAAGGATTCAT 1522
Db 1452 gctcagcttcttcttcttcttgagagaaacaataagaacataaaggaagagatctcat 1511
QY 1523 GTGGAATATPAAGAGGCTGACTTGTCTCTCTTCTTGGACTCTTGTTCAGTTTCAATTTCA 1582
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QY 1583 GTGCTGCTACTGATGACACACTTCTAATGAAGGCAAAATTTGATTCATATGGAATA 1642
Db 1572 gtgctgacttgatgacagacacttcaatgaagtgcaaatltgatacatatgtgaata 1631
QY 1643 TGACACTCAGTTTCTTTCAGATCAATTTTCAGGTGCTCTTGTATACGTGAGAGTACA 1702
Db 1632 tggactcagtttcttctgacgaatcaaatcttcaagtgctctctgtatactgtggaagtaca 1691
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QY 1943 ATAGCCTGCGGGTTTTTATGTTGGGGTTTTGCTGTTTCTTATGAGACCCATTC 2002
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QY 2003 TATTTCTTATGCAATGTTTCTTTATCAGATATTTTATGAGAAGAAACATCACTGAA 2062
Db 1991 tattctctatagtaactgttcttcttcttcttcttcttcttcttcttcttcttcttcttct 2050
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RESULT 2
US-60-278-2538
; Sequence 2538, Application US/60278258
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; TITLE OF INVENTION: Polymorphisms Identified Thereby
; FILE REFERENCE: GX-0010-1 P
; CURRENT APPLICATION NUMBER: US/60/278, 258
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 17730

Db 1441 atggcgtgacttgctctcttcttgactcttgcttcttcaagttcaatcagtcgtacttga 1500
QY 1596 TGACAGACACTTCTAAATGAGTGCATAATTTGATACATATGTGAAATATGAGCTCAGTTT 1655
Db 1501 tgcagagacactcctaaatgaaatgaaatcttgatacatatgataatgactcagttc 1560
QY 1656 CTTCGAGATCAAAATTTACGTCGCTCTCTATATCTGTGAGAGTACACTCTTATAGAAAG 1715
Db 1561 ctgcagatacaaatcttcaagctctctgatactgtaagtaacatcttataagaaag 1620
QY 1716 TTTCAAAAGTCTAGCT 1775
Db 1621 ttcataaagctacagct 1680
QY 1776 AGTTGAAAGTCTCTATTTTGACTGTAGCTCGCTGTGTGTAATTTGACCATCTATTT 1835
Db 1681 agttgaaagagct 1740
QY 1836 AACTGGCTTACGCT 1895
Db 1741 aactggtctca-gctcccaactctctctctctctctctctctctctctctctctctct 1799
QY 1896 CACACCTAGCATCTCATGAGTGGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1955
Db 1800 cacacctaagcatctcatgagtgccaagcaaaagagagagagagagagagagagagag 1859
QY 1956 TTTTGTATGTTGGGGGTTTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2015
Db 1860 tttttgattggggggttctgtctctctctctctctctctctctctctctctctctctct 1919
QY 2016 CAAATGTTCTTTTATCAGATATTTATTTAGTAAAGAAACATCAGTAATCTAGTCTCAA 2075
Db 1920 caatgttctcttct 1979
QY 2076 GTGACATCTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2135
Db 1980 gtgacatctcttct 2039
QY 2136 CAATGAAATGCT 2195
Db 2040 caatgaaatgct 2099
QY 2196 ATATTTCTTTAAATTTGATCTCAGGCTCGCTCAACCCAC 2235
Db 2100 atattcttcaatct 2139
RESULT 4
US-09-760-443-684
; Sequence 684, Application US/09760443
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ212
; CURRENT APPLICATION NUMBER: US/09/760,443
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2164
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 684
; LENGTH: 1213
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1114)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1121)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1142)
; OTHER INFORMATION: n equals a,t,g, or c

; NAME/KEY: SITE
; LOCATION: (1157)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1182)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-760-443-684
Query Match 49.5%; Score 1117.2; DB 6; Length 1213;
Best Local Similarity 96.5%; Pred. No. 1.1e-292;
Matches 1171; Conservative 9; Mismatches 27; Indels 6; Gaps 4;
QY 692 GCCCAGTGTACAGTTGATTCAGTGTGAGCTTTGGAGGCCCAAGCTGGTACCAT 751
Db 1 gcccaagtgtaagcttgatctcagtgatgagccttggagcccaagctgggttaacat 60
QY 752 GGAAGTACACACCCCTTGGAAACCTTACAGTTCAGCTTACAGTTCAGTTCAGTTCAGTTC 811
Db 61 ggaagtgtaagccttctgggaaacttcaagcttcaagcttcaagcttcaagcttcaagct 120
QY 812 TGAAGAAACAATTTAACTGGATTTGAAGAAACCACTGTGACATTTGAAACTGCTC 871
Db 121 tgaagaaacaacttcaagcttgatgagaaacacacttgagaccatttggaaactgctc 180
QY 872 ATCTCCGAACCAACTGCTGCAAGTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCT 931
Db 181 atctccgaacccaactgtaagctgagctgagctgagctgagctgagctgagctgagctg 240
QY 932 GATCATGACGTATGACATCCCTGCGACCTTACAGTTCAGTTCAGTTCAGTTCAGTTCAGT 991
Db 241 gatcatgacgtatgacatccctgcgaccttcaagcttcaagcttcaagcttcaagcttca 300
QY 992 CTGCTCAGAAAGAACTGATTAATTTGGAAGAAAGAAACCAATTTGTAATCATCTGGAAT 1051
Db 301 ctgctcagaagaaactgataatcttgagaaagaaacacatttgaatcatcttggaat 360
QY 1052 CTGCTCAATTCATAGTTCATATGTCAAAAATTTGACAAAAGTTTTCATGATTAAGA 1111
Db 361 ctgctcaatctcagcttcaatcttcaaaaatctgaaagaaatcttcaatcttcaatct 420
QY 1112 GGGGATTTATTAACCCCTCTTCAATTCAGTGGCAGTGTATGTTGATCTCTGTGCTT 1171
Db 421 ggggatatttaacccctcttcaatctcagtgagcaagtaagtaagtaagtaagtaag 480
QY 1172 GGCATTTATCATTTGGCTGGCAAGAGATTTAAAAAAGCAAGAAATCCAGAGAGATAT 1231
Db 481 ggcattatcatcttgctgctgcaagagattaaaaaagcaagaaatccaaagagagtat 540
QY 1232 GAATGACCCATATTAATTCGCCCTTGGTGAAGAAATTTCTTGAAATTAATTAATCATG 1291
Db 541 gaatgacccatatttaaatctgccccttggtaagaaatcttggaaatcttcaaaatct 600
QY 1292 AGATCTTTAAATTCCTTCATGAAAGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1351
Db 601 agatctttaaatcttctccttccttccttccttccttccttccttccttccttccttc 660
QY 1352 AAGTGTG-TTCTCTCAGTGTATGGAAGATTTCTACCCGACCAACAGTTCCTTACGCT 1410
Db 661 aagtggtg-ttctctcagtgatggaagatttctacccgacccaacagttcttcttcagct 720
QY 1411 TCCATTTGGCCCTCATATTTATCCCTCAACCCCAAGCCACAGGTGTTATTAACAGTCAAC 1470
Db 721 tccatttggccctcatatttccctcaaccccaagcccaaggttcttataagctcagc 780
QY 1471 TTTTGTCTTTTGAAGAGAAACAATAAGACAT-AAGGAAAGAGATTGATGATGAT 1529
Db 781 ttttgtcttttgaagagaaacaataagacataaagaaagaaatctcaatgagtaat 840
QY 1530 ATAAAGTGTGACTGATTTGCTCTTCTTCTGACTCTGTTTTCAGTTTCAATTCAGTGTCTG 1589
Db 841 ataaagtggtgactgatttct 900

QY	204	CTCTGTTGATGATTTCTTGCCACATCATGGAACCTACTGCTGAGACTTATATTCGAA	263
Db	270	ctctgttgatattcctctgacatcatatgaaacgcagctctgacttaaccattatctgaa	329
QY	264	AAACCCATGACGTGGCAAGGGCTTGAGAGATTCTGCCAGACATTACACAGATTTAAGTT	323
Db	330	aaacccatgaacacgcaagaagcttagaagattctgcgcgagcaaatiaacagatttagtt	389
QY	324	GCCATACAAACAGCGGAAATTGAGTATGTGGAGAAAGACTTGCCCTTCACATCGTCTT	383
Db	390	gccatacaaaacaagcggaaatttgagatctctggagaagactcgccttccagtgtct	449
QY	384	TACTACTGATGATGGAATCCGGAAGATAGAGAGATTATGACGTGGGTGGAGACCAACAA	443
Db	450	tactactgtgataggaaatccggaagataggaaatatgaaatcgtgtgtgtgaaaccaaaa	509
QY	444	TCTCTACATGAGAAGACGACAGAACCTGGGGAATGTGTAAGCCCAACAAAGAAAGAACAG	503
Db	510	tctcttactgaaagaagcagaaactctggggagatgtgtgaagcccaacaagaagaacaag	569
QY	504	GAGGACTGCGTGAGATCTATATCAAGAAACAAAGATGCAGGCAAAATGGAACGATGAC	563
Db	570	gagagactcgtgtgagatctatatacaagaacaagaatgcagcgaaatgtgaacagctgc	629
QY	564	GGCTGCGCAAAACCTTAAGGCGCCCTCTGTTACACAGCTTCTTGCCAGCCCTGTATCC	623
Db	630	gcccgcacaacaaactaaaggcagccctctgttaacacagctctcttgcagccctgtatgc	689
QY	624	AGTGCCATGAGAGATGTTGAATATCATCAATATATACAGCTGCACACTGTGTGAGGGG	683
Db	690	agtgccatgtgaagatgtgtgaataatcatcaataataataacccctgcaactcgtgtatgtggg	749
QY	684	TACTATGGGCCCCAGTGTCACTTGTGATTTCACTGATGAGCCCTTGTGAGGCCCCAGAGCTG	743
Db	750	tactatggccccagtgctcagytgtgtattcagtgltgaagcccttggaggccccagagctg	809
QY	744	GGTACCATGAGACTGATGACACCCCTTTGGAAACCTTCAGCTTCAGCTTCACAGTGTGCTTC	803
Db	810	ggtaccatgagactgtactcaccccttgggaaactcaagcttaagcttcaagatgtgccttc	869
QY	804	AGCTGCTCTGAAGAACAACTTAACGTGGATTGAGAAACCAACCTGTGGACCATTTGGA	863
Db	870	agctgctctgagaagaaacaacttaactcgtgatttgaagaacaacccctgtgaccatttga	929
QY	864	AACGTGCATATTCACAGAACCAACTGTGCAAGTATTCAGTGTGAGCCTTATACAGACCA	923
Db	930	aacgtgcataatccagaacaacactgttcaagtattcagtytgagccttatacaagcacaca	989
QY	924	GATTTGGGATCATGAACCTATAGCAATCCCTGGCCAGCTTCAGCTTAACTCTGACATGT	983
Db	990	gatttgggatacatgaactctgtagcaatccctcggcgcaagcttaagcttaaccctcgtcagtt	1049
QY	984	ACCTTCATCTGCTCAGAGGAACTGAGTTAATTTGGAGAGAGAAAAACATTTGTGAATCA	1043
Db	1050	accttcatactgtctagaagaagactgttaatttggagaagaagaacaacatttgaatca	1109
QY	1044	TCTGGAATCTGGTCAAACTCTACTGCCAATATGTGCAA	1080
Db	1110	tcgtgaatctgtgtcaaatctcttagtccaatatgtlcaaa	1146
RESULT 8			
US-09-760-443-575			
: Sequence 575, Application US/09760443			
GENERAL INFORMATION:			
: APPLICANT: Rosen et al.			
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies			
: FILE REFERENCE: PJ212			
: CURRENT APPLICATION NUMBER: US/09/760,443			
: CURRENT FILING DATE: 2001-01-16			
: Prior application data removed - refer to PALM or file wrapper			
NUMBER OF SEQ ID NOS: 2164			


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; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 210
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(579)
; OTHER INFORMATION: n = A,T,C or G
US-09-796-692-210
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Query Match          24.9%; Score 562.2; DB 6; Length 579;
Best Local Similarity 99.1%; Pred. No. 3.2e-142;
Matches 575; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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QY 1625 TTGATCATATGTAATGAGTACAGTTTCTTGCGAGATCAATTTACAGTGTCTTCT 1684
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DB 579 TTGATCATATGTAATGAGTACAGTTTCTTGCGAGATCAATTTACAGTGTCTTCT 520
QY 1685 GTATACGTGTGAGGTACACTCTTATAGAAAGTCAAAAAGTCAAGCTCTCTTTCTTC 1744
    |||||||
DB 519 GTATACGTGTGAGGTACACTCTTATAGAAAGTCAAAAAGTCAAGCTCTCTTTCTTC 460
QY 1745 TAACTCAGTGAAGTAATGGGGTCTGCTCAAGTGAAGAGTCTTATTTGCACTGTAGC 1804
    |||||||
DB 459 TAACTCAGTGAAGTAATGGGGTCTGCTCAAGTGAAGAGTCTTATTTGCACTGTAGC 400
QY 1805 CTCGGCGTGTGAATTTGGGCAATCCATTTAATGAGTCAAGGCTTCCAGCCACTTCTTC 1864
    |||||||
DB 399 CTCGGCGTGTGAATTTGGGCAATCCATTTAATGAGTCAAGGCTTCCAGCCACTTCTTC 341
QY 1865 AGCCACCTCTCTTTTTCAGTTGGCTGACTTCCACACCTTACATCTCATGTAGTGCAGCA 1924
    |||||||
DB 340 AGCCACCTCTCTTTTTCAGTTGGCTGACTTCCACACCTTACATCTCATGTAGTGCAGCA 281
QY 1925 AAAGGAGAGAGAGAGAAATAGCTCGCGGCTTTTGTAGTTGGGGTTTTGTCTTTC 1984
    |||||||
DB 280 AAAGGAGAGAGAGAGAAATAGCTCGCGGCTTTTGTAGTTGGGGTTTTGTCTTTC 221
QY 1985 TTTTATGAGACCCATTCCTATTCTTATATGTCATGTTCTTTTATACAGATATATTAG 2044
    |||||||
DB 220 TTTTATGAGACCCATTCCTATTCTTATATGTCATGTTCTTTTATACAGATATATTAG 161
QY 2045 TAAGAAACATCACTAAATAGTACGTCAAGTCAATCTCTTGTGATGTATGAGAGA 2104
    |||||||
DB 160 CAAGAAACATCACTAAATAGTACGTCAAGTCAATCTCTTGTGATGTATGAGAGA 101
QY 2105 GTTAAAAACAGGTGAGAAATTTCTTGATTCACAATGAATGCTCTCTTCCCTGCCCC 2164
    |||||||
DB 100 GTTAAAAACAGGTGAGAAATTTCTTGATTCACAATGAATGCTCTCTTCCCTGCCCC 41
QY 2165 CAGAAGTTTATCACTTACCTAGATTTCTATCATATTTCTTT 2204
    |||||||
DB 40 CAGAAGTTTATCACTTACCTAGATTTCTATCATATTTCTTT 1
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RESULT 12
US-09-796-692-4884/C
; Sequence 4884, Application US/09796692
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
; FILE REFERENCE: 2077, 001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 4884
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (511)
; OTHER INFORMATION: n=A,T,C or G
US-09-796-692-4884
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Query Match          24.9%; Score 562.2; DB 6; Length 579;
Best Local Similarity 99.1%; Pred. No. 3.2e-142;
Matches 575; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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QY 1625 TTGATCATATGTAATGAGTACAGTTTCTTGCGAGATCAATTTACAGTGTCTTCT 1684
    |||||||
DB 579 TTGATCATATGTAATGAGTACAGTTTCTTGCGAGATCAATTTACAGTGTCTTCT 520
QY 1685 GTATACGTGTGAGGTACACTCTTATAGAAAGTCAAAAAGTCAAGCTCTCTTTCTTC 1744
    |||||||
DB 519 GTATACGTGTGAGGTACACTCTTATAGAAAGTCAAAAAGTCAAGCTCTCTTTCTTC 460
QY 1745 TAACTCAGTGAAGTAATGGGGTCTGCTCAAGTGAAGAGTCTTATTTGCACTGTAGC 1804
    |||||||
DB 459 TAACTCAGTGAAGTAATGGGGTCTGCTCAAGTGAAGAGTCTTATTTGCACTGTAGC 400
QY 1805 CTCGGCGTGTGAATTTGGGCAATCCATTTAATGAGTCAAGGCTTCCAGCCACTTCTTC 1864
    |||||||
DB 399 CTCGGCGTGTGAATTTGGGCAATCCATTTAATGAGTCAAGGCTTCCAGCCACTTCTTC 341
QY 1865 AGCCACCTCTCTTTTTCAGTTGGCTGACTTCCACACCTTACATCTCATGTAGTGCAGCA 1924
    |||||||
DB 340 AGCCACCTCTCTTTTTCAGTTGGCTGACTTCCACACCTTACATCTCATGTAGTGCAGCA 281
QY 1925 AAAGGAGAGAGAGAGAAATAGCTCGCGGCTTTTGTAGTTGGGGTTTTGTCTTTC 1984
    |||||||
DB 280 AAAGGAGAGAGAGAGAAATAGCTCGCGGCTTTTGTAGTTGGGGTTTTGTCTTTC 221
QY 1985 TTTTATGAGACCCATTCCTATTCTTATATGTCATGTTCTTTTATACAGATATATTAG 2044
    |||||||
DB 220 TTTTATGAGACCCATTCCTATTCTTATATGTCATGTTCTTTTATACAGATATATTAG 161
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QY	2045	TAAAGAAAACATCACTGAAATGCTAGCGCGCAAGGACATCTCTTGATGTCATATGAGA	2104
Db	160	CAAGAAAACATCACTGAAATGCTAGCGCGCAAGGACATCTCTTGATGTCATATGAGA	101
QY	2105	GTAAACAGGTGAGAAATTCCTGTAATTCACAAATAAATGCTCTCTTCCCTGCCCC	2164
Db	100	GTAAACAGGTGAGAAATTCCTGTAATTCACAAATAAATGCTCTCTTCCCTGCCCC	41
QY	2165	CAGACCTTTATCCACTTACCTAGATTTCTACATATTCCTT	2204
Db	40	CAGACCTTTATCCACTTACCTAGATTTCTACATATTCCTT	1

RESULT 13
US-09-796-692-5257/c
; Sequence 5257, Application US/09796692

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1 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
2 OF INVENTION: HEMATOLOGICAL MALIGNANCIES
3 FILE REFERENCE: 2077 001200
4 CURRENT APPLICATION NUMBER: US/09/796,692
5 CURRENT FILING DATE: 2001-03-01
6 PRIOR APPLICATION NUMBER: 60/186,126
7 PRIOR FILING DATE: 2000-03-01
8 PRIOR APPLICATION NUMBER: 60/190,479
9 PRIOR FILING DATE: 2000-03-17
10 PRIOR APPLICATION NUMBER: 60/200,545
11 PRIOR FILING DATE: 2000-04-27
12 PRIOR APPLICATION NUMBER: 60/200,303
13 PRIOR FILING DATE: 2000-04-28
14 PRIOR APPLICATION NUMBER: 60/200,779
15 PRIOR FILING DATE: 2000-04-28
16 PRIOR APPLICATION NUMBER: 60/200,999
17 PRIOR FILING DATE: 2000-05-01
18 PRIOR APPLICATION NUMBER: 60/202,084
19 PRIOR FILING DATE: 2000-05-04
20 PRIOR APPLICATION NUMBER: 60/206,201
21 PRIOR FILING DATE: 2000-05-22
22 PRIOR APPLICATION NUMBER: 60/218,950
23 PRIOR FILING DATE: 2000-07-14
24 PRIOR APPLICATION NUMBER: 60/222,903
25 PRIOR FILING DATE: 2000-08-03
26 PRIOR APPLICATION NUMBER: 60/223,416
27 PRIOR FILING DATE: 2000-08-04
28 PRIOR APPLICATION NUMBER: 60/223,378
29 PRIOR FILING DATE: 2000-08-07
30 NUMBER OF SEQ ID NOS: 9597
31 SOFTWARE: fastseq for Windows Version 3.0
32 SEQ ID NO 5257

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? TYPE: DNA
? ORGANISM: Homo sapiens
?
? FEATURE:
?
? NAME/KEY: unsure
? LOCATION: (497)
? OTHER INFORMATION: n=A,T,C or G
US-09-796-692-5257

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Query Match	24.3%	Score 549.2;	DB 6;	Length 577;
Best Local Similarity	99.1%;	Pred. No. 1.1e-138;		
Matches 573; Conservative	0;	Mismatches 3;	Indels 2;	Gaps 2

QY 1628 ATGCAATGTGGAATATGAGCTACGTTTCTGTGAGATCAAAATTTGACGCGCTCTTGTA 1687
|||||
Db 577 ATGCAATGTGGAATATGAGCTACGTTTCTGTGAGATCAAAATTTGACGCGCTCTTGTA 518
QY 1688 TACGTGAGAGCTACACTCTT-ATAGAAATTTCAAAAAGCTACGCTCTTCTTTCTTA 1746
|||||

Db	517	TAAGTGGAGGTACACGCTTNTATGAAGAAGTCAAAAAGTCTACGCTCTCTTTCTTTCTA	458
QY	1747	ACTCCAGTGAAGTATATGGGGTCTGCTCAAGTTGAAAGAGTCTATTTSCACTGAGCTT	1806
Db	457	ACTCCAGTGAAGTATATGGGGTCTGCTCAAGTTGAAAGAGTCTATTTSCACTGAGCTT	398
QY	1807	CGCCCTGTGAATTTGGACCATCTTATTTTACTGGCTGACGGCTCCGACCTTCTTACG	1866
Db	397	CGCCCTGTGTGAATTTGGACCATCTTATTTTACTGGCTGACGGCTCCGACCTTCTTACG	339
QY	1867	CCACCTCTCTTTTTCAGTTGGTGACTTCCACACCTGACATCTCATGAGTSCCAAGCAA	1928
Db	338	CCACCTCTCTTTTTCAGTTGGTGACTTCCACACCTGACATCTCATGAGTSCCAAGCAA	279
QY	1927	AGGAGAGAAAGAGAAATTTATGCTGCGGGGTTTTTGTGGGGGTTTTGGCTGTTCCCT	1986
Db	278	AGGAGAGAAAGAGAAATTTATGCTGCGGGGTTTTTGTGGGGGTTTTGGCTGTTCCCT	219
QY	1987	TTATGAGACCCATTCCTATTTCTTTATAGTCAATGTTCTTTTATCAGATATTTATTAGTA	2046
Db	218	TTATGAGACCCATTCCTATTTCTTTATAGTCAATGTTCTTTTATCAGATATTTATTAGTA	159
QY	2047	AGAAACATCATCGAAATTCGTACTGTCAGTGCATCTTTGATGATCATATGGAAGGT	2106
Db	158	AGAAACATCATCGAAATTCGTACTGTCAGTGCATCTTTGATGATCATATGGAAGGT	99
QY	2107	TAAACAGGTGAGAAATTTCTTGATTTCACAATGAATGCTCTCTTCCCTGCCGCCCA	2166
Db	98	TAAACAGGTGAGAAATTTCTTGATTTCACAATGAATGCTCTCTTCCCTGCCGCCCA	39
QY	2167	GAACTTTTATTCACCTTACTGATGTTCTACATATTTCTTT	2204
Db	38	GAACTTTTATTCACCTTACTGATGTTCTACATATTTCTTT	1

RESULT 14
US-09-796-692-8471/c
; Sequence 8471, Application US/09796692

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1 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
2 TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
3 FILE REFERENCE: 2077_001200
4 CURRENT APPLICATION NUMBER: US/09/796,692
5 CURRENT FILING DATE: 2001-03-01
6 PRIOR APPLICATION NUMBER: 60/186,126
7 PRIOR FILING DATE: 2000-03-01
8 PRIOR APPLICATION NUMBER: 60/190,479
9 PRIOR FILING DATE: 2000-03-17
10 PRIOR APPLICATION NUMBER: 60/200,545
11 PRIOR FILING DATE: 2000-04-27
12 PRIOR APPLICATION NUMBER: 60/200,303
13 PRIOR FILING DATE: 2000-04-28
14 PRIOR APPLICATION NUMBER: 60/200,779
15 PRIOR FILING DATE: 2000-04-28
16 PRIOR APPLICATION NUMBER: 60/200,999
17 PRIOR FILING DATE: 2000-05-01
18 PRIOR APPLICATION NUMBER: 60/202,084
19 PRIOR FILING DATE: 2000-05-04
20 PRIOR APPLICATION NUMBER: 60/206,201
21 PRIOR FILING DATE: 2000-05-22
22 PRIOR APPLICATION NUMBER: 60/218,950
23 PRIOR FILING DATE: 2000-07-14
24 PRIOR APPLICATION NUMBER: 60/222,903
25 PRIOR FILING DATE: 2000-08-03
26 PRIOR APPLICATION NUMBER: 60/223,416
27 PRIOR FILING DATE: 2000-08-04
28 PRIOR APPLICATION NUMBER: 60/223,378
29 PRIOR FILING DATE: 2000-08-07
30 NUMBER OF SEQ ID NOS: 9597
31 SOFTWARE: FastSeq for Windows Version 3.0

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2001, 23:18:21 ; Search time 2226.75 seconds
(without alignments)
9589.759 Million cell updates/sec

Title: US-09-119-209-1

Perfect score: 2259

Sequence: 1 GAATTCAGTGTGCTGCTT.....CCGCCAGCACACTGGAATTC 2259

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 segs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

DB	Accession	Source	Score	DB	Length
DB	542 CTGCAACAACTAAGGACACCCCTGTTACACAGCTCTTGGCAGGCCCTGTCATGCCA	601			
QY	625 GTGGCCATGAGAGATGTGTGAATATCATATATACACCTGCACACTGTGATGGGGT	684			
DB	602 GTGGCCATGAGAGATGTGTGAATATCATATATACACCTGCACAGTGATGGGGT	661			
QY	685 ACTATGAGGCCCCGAGTGCACCTGTGATTAAGTGTAGGCGCTTTGGAGGCCAGAGGTGG	744			
DB	662 ACTATGAGGCCCCGAGTGCACCTGTGATTAAGTGTAGGCGCTTTGGAGGCCAGAGGTGG	720			
QY	745 GTACATATGAGCT-GTACTACACCCCTTTGGAACCTTCAGCTTACAGTGCAGTGTGCCTTC	803			
DB	721 GTACATATGAGCTGTGTTCTACCTTTGGGCAAACTTACGCTTACACTACAGTGTGTCTT	780			
QY	804 AGCTGCTCTGAGAGAACAA 822				
DB	781 CAGTGTCTGAGAGAACAA 799				
RESULT	2				
LOCUS	BS541944	739 bp	MRNA	EST	03-APR-2001
DEFINITION	602569447F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4694194 5',				
ACCESSION	BS541944				
VERSION	BS541944.1	GI:13534177			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 739)				
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cga@rs-remail.nih.gov				
	Tissue procurement: Clontech Laboratories, Inc.				
	cDNA Library Preparation: Clontech Laboratories, Inc.				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
	DNA Sequencing by: Incyte Genomics, Inc.				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LLNL at:				
	http://image.llnl.gov				
	Plate: L1CMI517 row: m column: 11				
	High quality sequence stop: 716.				
FEATURES	Location/Qualifiers				
source	1..739				
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	/db_xref="taxon:9606"				
	/clone="IMAGE:4694194"				
	/clone_id="NIH_MGC_77"				
	/lab_host="DH10B (TI phage-resistant)"				
	/note="Organ: Lung; Vector: pMDR-LIB (Clontech); Site:1:				
	sfiI (ggcgccctggcc); Site:2: sfiI (ggcattatggcc); 5' and				
	3' adaptors were used in cloning as follows: 5' adaptor				
	sequence: 5'-CACGCGCATTTGCGC-3' and 3' adaptor sequence				
	5'-ATTCTAGAGCGCGAGCGCGCACATG-dT(30)BN-3' (where B = A,				
	C, or G and N = A, C, G, or T). Average insert size 1.9				
	kb (range 0.5-4.0 kb). 12/15 colonies contained inserts				
	by PCR. This library was enriched for full-length clones				
	and was constructed by Clontech Laboratories (Palo Alto,				
	CA). Note: this is a NIH-MGC Library."				
BASE COUNT	223 a 157 c 198 g 161 t				
ORIGIN					
Query Match	29.0%; Score 654.4; DB 155; Length 739;				
Best Local Similarity	98.6%; Pred. No. 2.3e-174;				
Matches 702; Conservative	0; Mismatches 6; Indels 4; Gaps 4;				
25	ACGCGACGACGACGACCTCCCTT-GGCAAGGACCTGAGACCCCTTGGCTTAAGTCAGAA	83			

D	b		25	ACCTGAGCAGACGACACTCCCTTTGGGCAAGAACCTGTGAACCCCTTGTGTAAGTAA	84
O	y		84	GGCTCAATGGGCTGCAGAAGAACTAGAGAAGACCAAGCAAGCCATGATATTTCATG	143
D	b		85	GGCCTAATGGGCTGCAGAAGAACTAGAGAAGACCAAGCAAGCCATGATATTTCATG	144
O	y		144	AAATGTCAGAGCACCCAGAGGACTTATGGAACATCTTCAAAGTTTGCGGGTGGACATG	203
D	b		145	AAATGTCAGAGCACCCAGAGGACTTATGGAACATCTTCAAAGTTTGCGGGTGGACATG	204
O	y		204	CTCTGTTGATTTTCCTGGCACATCATGGAACCACTGACCTGAGCTTACCATTATTCGAA	263
D	b		205	CTCTGCTGTGATTTTCCTGGCACATCATGGAACCACTGACCTGAGCTTACCATTATTCGAA	264
O	y		264	AAACCCATGAACCTGGCAAAAGGGCTAGAAAGTTCTGCCGAGACAATTACACAGATTAGTT	323
D	b		265	AAACCCATGAACCTGGCAAAAGGGCTAGAAAGTTCTGCCGAGACAATTACACAGATTAGTT	324
O	y		324	GGCATACAAAACAAGGGGGAATATGATATCTGSAGAAAGCTTGCCCTTCACTGCTTCT	383
D	b		325	GGCATACAAAACAAGGGGGAATATGATATCTGSAGAAAGCTTGCCCTTCACTGCTTCT	384
O	y		384	TACTCTGTGATAGGAATCCGGAAGATAGAGGAATATGACCTGGGTGGGAACCAACAA	443
D	b		385	TACTCTGTGATAGGAATCCGGAAGATAGAGGAATATGACCTGGGTGGGAACCAACAA	444
O	y		444	TCTCTCACTGAAGAAGCAGAGAACTGGGGAGATGTGAGGCCCAACAACAAGAAGAACAG	503
D	b		445	TCTCTTACTGAAGAAGCAGAGAACTGGGGAGATGTGAGGCCCAACAACAAGAAGAACAG	504
O	y		504	GAGAGCTCGGAGGAGATCTATATCAAGAAACAAAGATCGAAGCAAAATGGAACATGAC	563
D	b		505	GAGAGCTCGGAGGAGATCTATATCAAGAAACAAAGATCGAAGCAAAATGGAACATGAC	564
O	y		564	GCTTCGCCAACAACATAAGAGCAGCCCTGTGTACACAGCTTCTGGCCAGCCGCTGATGAC	623
D	b		565	GCTTCGCCA - AAACATAAGGACGCCCTGTGTACACAGCTTCTGGCCAGCCGCTGATGAC	623
O	y		624	AGTGGCCATGAGAGATGTGTAGAAATCATCATATACACCTGCAACTGTGATGTGGGG	683
D	b		624	AGTGGCCATGAGAGATGTGTAGAAATCATCATATACACCTGCAACTGTGATGTGGGG	682
O	y		684	TACTATGGGGCCCCAGTGCAGCTTGATCATGATGAGCTTGGAGGCC	735
D	b		683	TACTATGGGGCCCCAGTGCAG - TTGTGATTCAGTGTGAGCCCTTTGGAGGCC	733

RESULT	3				
LOCUS	AM950859	621 bp	mRNA	EST	01-JUN-2000
DEFINITION	EST362929 MAGE resequences, MAGA Homo sapiens cDNA, mRNA sequence.				
ACCESSION	AM950859				
VERSION	AM950859.1	GI:8140521			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 621)				
AUTHORS	Hegde,P., Ol,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holtz,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.				
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: john@etlgr.org Plate: 20 Seq primer: Reverse.				

FEATURES		Location/Qualifiers	
SOURCE		1. 621	
		/organism="Homo sapiens"	
		/db_xref="taxon:9606"	
		/clone_11b="MAGE resesquences, MAGE"	
		/note="Vector: plbuescripts.m"	
BASE COUNT	172 a 135 c 119 g 194 t	1 others	
ORIGIN			
Query Match	26.2%; Score 592.8; DB 122; Length 621;		
Best Local Similarity	99.4%; Pred. No. 6.6e-157;		
Matches	616; Conservative 0; Mismatches 2; Indels 2; Gaps 2;		
QY	1210 GCACAGAAATCCAGAGAGATGTAATGACCCATATTAAATGCGCCCTGGTGAAGAAAT	1269	
Db	1 GCACAGAAATCCAGAGAGATGTAATGAGACCATATTAAATGCGCCCTGGTGAAGAAAT	60	
QY	1270 TCTTGGAACTACTAAAAATCATGAGATCCCTTTAAATCCTTCCATGAACGTTTGTGTGT	1329	
Db	61 TCTTGGAACTACTAAAAATCATGAGATCCCTTTAAATCCTTCCATGAACGTTTGTGTGT	120	
QY	1330 GGCACCTCTACGTCAAAACATGAACTGTG-TCCTTCAGTGCATGTGGAGATTTCTAC	1388	
Db	121 GGCACCTCTCTACGTCAAAACATGAACTGTGTCTTCCTTCAGTGCATGTGGAGATTTCTAC	180	
QY	1389 CCGACCAACAGTTCCTTCAGCTTCATTTGCGCCCTCAATTAATCCCTCAACCCGAGCC	1448	
Db	181 CCGACCAACAGTTCCTTCAGCTTCATTTGCGCCCTCAATTAATCCCTCAACCCGAGCC	240	
QY	1449 ACAGTGTTTATACAGCTCAGCTTTTGTCTTTCTGAGAGAAACAATAAGACCAT-A	1507	
Db	241 ACAGTGTTTATACAGCTCAGCTTTTGTCTTTCTGAGAGAAACAATAAGACCATAA	300	
QY	1508 AGGGAAGAGATTCAATGAGGAATTAAGATGGCTGACTTGTCTTTGACCTGTGT	1567	
Db	301 AGGGAAGAGATTCAATGAGGAATTAAGATGGCTGACTTGTCTTTGACCTGTGT	360	
QY	1568 TTCACTTTCAATTCAGTCTGCTACTTGTATGACAGACACTTCTAAATGAAGTCAAAATTG	1627	
Db	361 TTCACTTTCAATTCAGTCTGCTACTTGTATGACAGACACTTCTAAATGAAGTCAAAATTG	420	
QY	1628 ATACATATGTGAATATGACATCAGTCTTCTTCGACATCAAAATTCAGCTGCTTCTGTA	1687	
Db	421 ATACATATGTGAATATGACATCAGTCTTCTTCGACATCAAAATTCAGCTGCTTCTGTA	480	
QY	1688 TACCTGTGAGGTACACCTCTTATAGAAATTTCAAAAAGCTACGCTCTCTTTCTTAA	1747	
Db	481 TACCTGTGAGGTACACCTCTTATAGAAATTTCAAAAAGCTACGCTCTCTTTCTTAA	540	
QY	1748 CTCACGTAAGTAATGGGGTCTGCTCAAGTTGGAAGAAGTCTATTTCACGTGACGCTC	1807	
Db	541 CTCACGTAAGTAATGGGGTCTGCTCAAGTTGGAAGAAGTCTATTTCACGTGACGCTC	600	
QY	1808 GCCGTGTGTGAATTGGACCA	1827	
Db	601 GCCGTGTGTGAATTGGACCA	620	
RESULT	4		
AM408490			
LOCUS	551 bp mRNA	EST	16-FEB-2000
DEFINITION	UI-HF-BKO-adm-g-01-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone		
IMAGE	3056832 5', mRNA sequence.		
ACCESSION	AM408490		
VERSION	AM408490.1 GI:6927547		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheraia; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 551)		
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/ .		

TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaabs@email.nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.lnl.gov/bbrp/image/image.html Seq primer: M13 forward. Location/Qualifiers
FEATURES	Location/Qualifiers
source	1..551 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:3056832" /clone_1lp="NIH-MGC_36" /tissue_type="Lymph" /cell_type="germinal center B cells" /cell_line="MGC85" /lab_host="DH10B (LTR)" /note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT	162 a 124 c 106 g 159 t
ORIGIN	
Query Match	23.5%; Score 531.4; DB 115; Length 551;
Best Local Similarity	99.6%; Pred. No. 1.7e-139;
Matches 543; Conservative	0; Mismatches 1; Indels 1; Gaps 1;
OY 961	GCTTCAGCTTACCTCTGCATGTACCTTCATCTGCTCGAAGAAGCTGATTAATGGGA 1020
Db 7	GCTTCAGCTTACCTCTGCATGTACCTTCATCTGCTCGAAGAAGCTGATTAATGGGA 66
OY 1021	AGAGAAACCATTTGTAATCATCTGGAATCTGTCAAATCTAGTCCATATGTCAA 1080
Db 67	AGAGAAACCATTTGTAATCATCTGGAATCTGTCAAATCTAGTCCATATGTCAA 126
OY 1081	AATGGACAAGAGTTTTCATATGATTAAGAGAGGATTAATACCCCTCTTATCCAG 1140
Db 127	AATGGACAAGAGTTTTCATATGATTAAGAGAGGATTAATACCCCTCTTATCCAG 186
OY 1141	TGGCAGTCATGTTACTGCATTTCTGTGGTTGGCATTTATCATTTGGCTGGCAAGAGAT 1200
Db 187	TGGCAGTCATGTTACTGCATTTCTGTGGTTGGCATTTATCATTTGGCTGGCAAGAGAT 246
OY 1201	TAAAAAAGGCAAGAAATCCAAAGAGAGATATGATGACCCATATTAATGCCCTTGGTG 1260
Db 247	TAAAAAAGGCAAGAAATCCAAAGAGAGATATGATGACCCATATTAATGCCCTTGGTG 306
OY 1261	AAAGAAATTTCTTGGAAATACATAAAATATGAGATCCCTTAAATCCTTCATGAAGAGCTT 1320
Db 307	AAAGAAATTTCTTGGAAATACATAAAATATGAGATCCCTTAAATCCTTCATGAAGAGCTT 366
OY 1321	TTGTGTGTGGCACCCTCTACGTCAAAACATGAAGTGTG-TTCCTTCAGTGCATCTGGAA 1379
Db 367	TTGTGTGTGGCACCCTCTACGTCAAAACATGAAGTGTG-TTCCTTCAGTGCATCTGGAA 426
OY 1380	GATTTCTACCCGACCAAGTTCCTTCAGCTTCATTTGGCCCTCATTTATCCCTCAAC 1439
Db 427	GATTTCTACCCGACCAAGTTCCTTCAGCTTCATTTGGCCCTCATTTATCCCTCAAC 486
OY 1440	CCCCAGCCCAAGGTTTATACAGCTAGCTTTTGTCTTTTGTGAGAGAGAAACAATA 1499
Db 487	CCCCAGCCCAAGGTTTATACAGCTAGCTTTTGTCTTTTGTGAGAGAGAAACAATA 546
OY 1500	AGACC 1504

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Db      547 AGACC 551

RESULT  5
BF790688      876 bp      mRNA      EST      12-JAN-2001
LOCUS      602250524F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4338268 5',
DEFINITION      mRNA sequence.
ACCESSION      BF790688
VERSION      BF790688.1 GI:12095742
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabs-remail.nih.gov
              Tissue Procurement: CLONTECH Laboratories, Inc.
              cDNA Library Preparation: CLONTECH Laboratories, Inc.
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              plate: LLCM1213 row: 0 column: 05
              High quality sequence stop: 549.
FEATURES
    source
        1. 876
            location/Qualifiers
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            /db_xref="taxon:9606"
            /clone_1ib="NIH_MGC_81"
            /lab_host="DH10B (T1 phage-resistant)"
            /note="Organ: muscle (skeletal); Vector: pDNR-LIB
            (Clontech); Site:1: SfiI (ggccgctcgcc); Site:2: SfiI
            (ggccatagcc); 5' and 3' adaptors were used in cloning
            as follows: 5' adaptor sequence: 5'-CACGCCCATATAGGCC-3'
            and 3' adaptor sequence:
            5'-ATTCTAGAGCGGAGCGCGCACATG-dT(30)BN-3' (where B = A,
            C, or G and N = A, C, G, or T). Average insert size
            1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
            inserts by PCR. This library was enriched for full-length
            clones and was constructed by Clontech Laboratories (Palo
            Alto, CA)."
BASE COUNT      229 a      205 c      250 g      192 t
ORIGIN
Query Match      22.6%; Score 511.4; DB 169; Length 876;
Best Local Similarity 94.2%; Pred. No. 9,6e-134;
Matches 585; Conservative 0; Mismatches 31; Indels 5; Gaps 5;
QY      25 ACTGCAGACAGACACTCCCTTGGCAAGACCTGAGACCTTGCTAAGTCAAG 84
      |||||||
Db      11 ACTGCAGACAGACACTCCCTTGGCAAGACCTGAGACCTTGCTAAGTCAAG 69
QY      85 GCTCAATGGGCTGCGAGAGACTAGAGAGAACCAAGCAAGCCATGATATTTCCATGA 144
      |||||||
Db      70 GCTCAATGGGCTGCGAGAGACTAGAGAGAACCAAGCAAGCCATGATATTTCCATGA 129
QY      145 AATGTCAGAGCAACAGAGAGACTATGAGACATCTTCAAGTTGGGGGTGAGACAATGC 204
      |||||||
Db      130 AATGTCAGAGCAACAGAGAGACTATGAGACATCTTCAAG-TGTGGGGGTGAGACAATGC 188
QY      205 TCTGTGTGATTTCTTGCGACATCATGGAACCTACTGCTGAGCTTACCTATTTCTGAAA 264
      |||||||
Db      189 TCTG-TGTGATTTCTTGCGACATCATGGAACCGACTGCTGAGCTTACCTATTTCTGAAA 247

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QY      265 AACCCATGACTGGCAAGAGGCTGAGAAATTCGCCGAGCAATTCACAGATTAGTTG 324
      |||||||
Db      248 AACCCATGAACTGGCAAGAGGCTGAGAAATTCGCCGAGCAATTCACAGATTAGTTG 307
QY      325 CCATACAAACAAAGCGGAAATTGATATCTGAGAGAACTGCTGCCCTGCTTCTT 384
      |||||||
Db      308 CCATACAAACAAAGCGGAAATTGATATCTGAGAGAACTGCTGCCCTGCTTCTT 367
QY      385 ACTACTGGATAGGAATCCGGAAGATAGAGAAATATGACAGCTGGTGGGACCAACAAAT 444
      |||||||
Db      368 ACTACTGGATAGGAATCCGGAAGATAGAGAAATATGACAGCTGGTGGGACCAACAAAT 427
QY      445 CTCTCACTGAAGAAGCAGAGAACTGGGAGATGAGTGCACCAACCAAGAAACAAAG 504
      |||||||
Db      428 CTCTCACTGAAGAAGCAGAGAACTGGGAGATGAGTGCACCAACCAAGAAACAAAG 487
QY      505 AGGACTGCGTGGAGATCTATATCAAGAGAAACAAAGATGAGGCAATGGAACGATGAG 564
      |||||||
Db      488 AGGACTGCGTGGAGATCTATATCAAGAGAAACAAAGATGAGGCAATGGAACGATGAG 546
QY      565 CCTGCCACAACATAAAGGACCCCTGTTACACAGCTTCTGCCAGCCCTGCTCATGCA 624
      |||||||
Db      547 CCTGCCACAACATAAAGGACCCCTGTTACACAGCTTCTGCCAGCCCTGCTCATGCA 605
QY      625 GTGGCCATGGAGAAATGTGAG 645
      |||||||
Db      606 GTGGCTGGGATGGGGTGAAG 626

RESULT  6
AM075834/c      632 bp      mRNA      EST      13-OCT-1999
LOCUS      xa80c03.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573092 3',
DEFINITION      similar to gb:X16150_cds1 L-SELECTIN PRECURSOR (HUMAN);, mRNA
              sequence.
ACCESSION      AM075834
VERSION      AM075834.1 GI:6030832
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
              1 (bases 1 to 632)
AUTHORS      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              Unpublished (1997)
JOURNAL      Contact: Robert Strausberg, Ph.D.
COMMENT      Email: cgabs-remail.nih.gov
              Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,
              Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
              Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
              I.M.A.G.E. Consortium DNA Sequencing by: Washington University
              Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html
              Seq primer: -40bp from Glibco
              High quality sequence stop: 147.
FEATURES
    source
        1. 632
            location/Qualifiers
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:2573092"
            /clone_1ib="NCI_CGAP_CML1"
            /tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL
            rearrangement positive, includes both chronic phase and
            myeloid blast crisis"
            /lab_host="DH10B"
            /note="Organ: whole blood; Vector: pCMV-SPORT6; Site:1:
            Sall; Site:2: NotI; Cloned unidirectionally. Primer":
            0190 dT. Library constructed by Life Technologies."
BASE COUNT      175 a      126 c      130 g      201 t

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Oy	1731	-	-CTCCGCTTTCCTTTCAATCCAGTAGAATAAGGGGTCTCGTCAAGTTGAAGA	1785
Db	598	CTCTCCTTTTCTACTACAACTCCAGTAGAAGTAAGGAGGTCACAGTCGAACA	657	
Oy	1786	GTCCTATTGCACCTAGCCCTCCGCTCTGTGTGAATTGAGCATATC	1829	
Db	658	GTTCTATTATGCACTGGTAGCGCTCGCGCTGTGAATGTGACATATC	701	
RESULT	8			
BGS31689				
LOCUS	BGS31689	946 bp	mRNA	EST
DEFINITION	602560237F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4698320	5'		03-APR-2001
ACCESSION	BGS31689			
VERSION	BGS31689.1	GI:13523227		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	NIH-MGC http://mgc.ncl.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: ILCLM1528 row: i column: 09 High quality sequence stop: 551. Location/Qualifiers 1..946 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4698320" /clone_id="NIH_MGC_61" /tissue_type="embryonal carcinoma" /lab_host="DH10B (TI phage-resistant)" /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1 SfiI (ggccgcttcgcgc); Site_2 SfiI (ggccattagcgc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGGCCGCGCGCGCATG-drr(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC library."			
FEATURES				
SOURCE				
BASE COUNT	279 a	186 c	292 g	189 t
ORIGIN				
Query Match	19.0%;	Score 429.4;	DB 154;	Length 946;
Best Local Similarity	84.5%;	Pred. No. 1.9e-110;		
Matches 601,	Conservative	0;	Mismatches 96;	Indels 14;
			Gaps	10;
Oy	25	ACCTGCACACAGCACACTCCCTT-GGCAGAGACCTGAGACCCTTGTCCTAAGTCACA	83	
Db	72	ACCTGCACACAGCACACTCCCTTGGGCAAGAGACCTGAGACCTTGTCCTAAGTCACA	131	
Oy	84	GGCTCAATGGGCTGCA-CAGAACTAGAGAAAGGACCAAGCAAAGCATATTTCCATG	142	
Db	132	GGCTCAATGGGCTGCAAGAACACTAGAGAAAGGACCAAGCAAAGCATATTTCCATG	191	

OY	143	GAATGTGAGACAGACCACCAAGGACTTTATGGAACATCTTCAAGTTGTGGGGTGACAAAT	202
Db	192	GAATGTGAGACAGACCACCAAGGACTTTATGGAACATCTTCAAGTTGTGGGGTGACAAAT	251
OY	203	GCTGTGTTGATTTTCTGGCACATCATGGAACCTACTGCTGGACTTACATATATCTG-	261
Db	252	GCTGTGTTGATTTTCTGGCACATCATGGAACCTACTGCTGGACTTACATATATCTG	311
OY	262	AAAAAACCATGAACCTGGCAAAAGGCTAGAAATTTCTCCGAGACAATTAACAGATTTAG	321
Db	312	AAAAAACCATGAACCTGGCAAAAGGCTAGAAATTTCTCCGAGACAATTAACAGATTTAG	371
OY	322	TTGGCATACAAACCAAGGGGGAATTTGA-GTATCTGGGAANACCTCCCTTCAGTGTGT	380
Db	372	TTGGCATACAAACCAAGGGGGAATTTGA-GTATCTGGGAANACCTCCCTTCAGTGTGT	431
OY	381	TCTTACTACTGATATGGAATCCGGAAGATAGAG-GAATATGAGCTGGGTGGGAACAA	439
Db	432	TCTTACTACTGATATGGAATCCGGAAGATAGAGCGGAATATGAGCTGGGTGGGAACAA	491
OY	440	CAAAATCTCTACTG--AAGAAAGCAGAGAAGCTGGGAGATGGTAGCCCAACAAACAAGAG	497
Db	492	AAAATCTCTTACTGGAAGCAAGACAGAGAAGCTGGGAGATGGTAGCCCAACAAAGAAGA	551
OY	498	AACAAGAGAGACTGCGTGGAGATCTATATCAAGAG--AAACAAGATGCAAGCAATAGG	554
Db	552	ACGCGAGGAGAGACTGCGTGGAGATCTATATTTAAAGAGAACAAGAAATTTGCAAGCAATAGG	611
OY	555	AACGATGAGCGCTCGCAACAACTAAAGCAGAGCCCTCTATTAC--ACAGCTTCTGGCAGC	612
Db	612	GCACCGATGAGCCTTGCACAAAAGTTAAGGGGAGGCCCTTCGCTACCGGCACCTTCTTGGCAGG	671
OY	613	CTGTGTCATGCAAGTGGCCAGAGAAATGTGTGAATATCATATATACACTGCAACT	672
Db	672	CC-GGTGCTGCAAGTGAACATGGCCGAGCCGGGTGAATATCTCAAGAATTTGAACGGGAATG	730
OY	673	GTGA-TGTGGGGTACTATGGGCCCAAGTGTGACCTTGTGATTCAGTGTGAG	722
Db	731	GTGAGCGTTGGGTACTGTGGCCCAAGTGTGAAGTGTGATGAGTGAAGTGAACCTTGAAG	781

REFERENCE	TITLE	COMMENT
AA669146/c	LOCUS	
AA669146	DEFINITION	
ad94c05.s1	ACCESSION	
IMAGE:854600.3	VERSION	
AA669146	KEYWORDS	
AA669146.1	SOURCE	
GI:2630645	ORGANISM	
EST.		
human.		
Homo sapiens		
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;		
Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.		
1 (bases 1 to 575)		
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,		
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,		
White, Y., Wyllie, T., Waterston, R., and Wilson, R.		
WashU-NCI human EST Project		
Unpublished (1997)		
Contact: Wilson RK		
Washington University School of Medicine		
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
Tel: 314 286 1800		
Fax: 314 286 1810		
Email: est@watson.wustl.edu		
This clone is available royalty-free through LNL ; contact the		
IMAGE Consortium (info@image.jnl.gov) for further information.		
Seq primer: -00mj fwd. ER from Amersham		
High quality sequence stop: 473.		
Location/Qualifiers		
1..575		
/organism="Homo sapiens"		

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/db_xref="taxon:9606"
/clone_lib="Stratagene Lung (#937210)"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: lung; Vector: Bluescript SK-; Site_1: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: oligo
dt. normal lung. Average insert size: 1.0 Kb; Uni-2AP XR
vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."
BASE COUNT      197 a      90 c      146 g      142 t
ORIGIN

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Query Match      18.9%; Score 426.4; DB 10; Length 575;
Best Local Similarity 98.2%; Pred. No. 1.1e-109;
Matches 442; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

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QY 1786 GTCTATTGTCAGTGTAGCTGCGCTGTGTGATTTGGACATCTTAACTGGCTTC 1845
      |||||||
DB 575 GTCTATTGTCAGTGTAGCTGCGCTGTGTGATTTGGACATCTTAACTGGCTTC 518
      |||||||
QY 1846 AGGCTCCACCTCTTTCAGCCACTCTTTTCAGTTGGCTGACCTCCACCTAGC 1905
      |||||||
DB 517 CAGCCCTCCACCTCTTTCAGCCACTCTTTTCAGTTGGCTGACCTCCACCTAGC 458
      |||||||
QY 1906 ATCTCATGTAGTGCAGCAAGCAAGAGAGAGAAATAGCCCTGCGGTTTTTAACTT 1965
      |||||||
DB 457 ATCTCATGTAGTGCAGCAAGCAAGAGAGAGAAATAGCCCTGCGGTTTTTAACTT 398
      |||||||
QY 1966 TGGGGTTTTGCTGTTTCTTTTATGAGACCCATTTCTTATTTATGCAATGTTTC 2025
      |||||||
DB 397 TGGGGTTTTGCTGTTTCTTTTATGAGACCCATTTCTTATTTATGCAATGTTTC 338
      |||||||
QY 2026 TTATATCAGATATTATTAGTAAGAAACATCATGTAATGCTGCAAGTACATCTC 2085
      |||||||
DB 337 TTATATCAGATATTATTAGTAAGAAACATCATGTAATGCTGCAAGTACATCTC 218
      |||||||
QY 2086 TTATATCAGATATTATTAGTAAGAAACATCATGTAATGCTGCAAGTACATCTC 2145
      |||||||
DB 277 TTATATCAGATATTATTAGTAAGAAACATCATGTAATGCTGCAAGTACATCTC 218
      |||||||
QY 2146 CTCTCTCTTCCCTGCGCCAGACATTTATGCACTTACCTACATTTCTTTA 2205
      |||||||
DB 217 CTCTCTCTTCCCTGCGCCAGACATTTATGCACTTACCTACATTTCTTTA 158
      |||||||
QY 2206 AATTTATCTCAAGGCTGCTCAACCCAC 2235
      |||||||
DB 157 AATTTATCTCAAGGCTGCTCAACCCAC 128
      |||||||

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RESULT 10
BG236008/c 567 bp mRNA EST 12-FEB-2001
LOCUS      BG236008
DEFINITION BG236008 Homo sapiens cDNA clone IMAGE:4141700 3',
            mRNA sequence.
ACCESSION  BG236008.1 GI:12749855
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncilogap.
            1 (bases 1 to 567)
AUTHORS    Tumor Gene Index
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Unpublished (1997)
TITLE      Contact: Robert Strausberg, Ph.D.
            Email: cga@bbs-riemail.nih.gov
            Tissue Procurement: M. Bento Soares, Ph.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D. and M.Fatima

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Bonafido, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Seq primer: -40UP from Glibco
High quality sequence stop: 479.
Location/Qualifiers
1. 567
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Stratagene Lung (#937210)"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: lung; Vector: Bluescript SK-; Site_1: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: oligo
dt. normal lung. Average insert size: 1.0 Kb; Uni-2AP XR
vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."
BASE COUNT      191 a      88 c      142 g      146 t
ORIGIN

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Query Match      18.6%; Score 419.8; DB 175; Length 567;
Best Local Similarity 99.3%; Pred. No. 8.1e-108;
Matches 432; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 1801 TACCTGCGCGTGTGTAATGAGACATCTTAACTGCTTACGCGCTCCACCTT 1860
      |||||||
DB 567 TACCTGCGCGTGTGTAATGAGACATCTTAACTGCTTACGCGCTCCACCTT 509
      |||||||
QY 1861 CTTCAGCCACTCTCTTTTTCAGTGTGCTACTTCCACACTAGCATCTATGATGCCA 1920
      |||||||
DB 508 CTTCAGCCACTCTCTTTTTCAGTGTGCTACTTCCACACTAGCATCTATGATGCCA 449
      |||||||
QY 1921 AGCAAAAGAGAGAGAGAGAGAAATAGCCCTGCGGTTTTTAACTGCGGTTTGGCTGT 1980
      |||||||
DB 448 AGCAAAAGAGAGAGAGAGAGAAATAGCCCTGCGGTTTTTAACTGCGGTTTGGCTGT 369
      |||||||
QY 1981 TTCTTTTATGAGACCCATCTTCTTATGTAATGCTGCAATGCTTCTTTATCAGATATTA 2040
      |||||||
DB 388 TTCTTTTATGAGACCCATCTTCTTATGTAATGCTGCAATGCTTCTTTATCAGATATTA 329
      |||||||
QY 2041 TTATGTAAGAAACATCATGTAATGCTAGCTGCAAGTACATCTCTTTGATGTCATATGG 2100
      |||||||
DB 328 TTATGTAAGAAACATCATGTAATGCTAGCTGCAAGTACATCTCTTTGATGTCATATGG 269
      |||||||
QY 2101 AAGAGTTAAACAGGTGAGAAATTCCTTGATTCACATGAATGCTCTTCCCTG 2160
      |||||||
DB 268 AAGAGTTAAACAGGTGAGAAATTCCTTGATTCACATGAATGCTCTTCCCTG 209
      |||||||
QY 2161 CCCCAGAACTTTTATCAGTACTAGATTTACATATCTTTAAATTCATCTCAGGC 2220
      |||||||
DB 208 CCCCAGAACTTTTATCAGTACTAGATTTACATATCTTTAAATTCATCTCAGGC 149
      |||||||
QY 2221 CTCTCTCAACCCAC 2235
      |||||||
DB 148 CTCTCTCAACCCAC 134
      |||||||

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RESULT 11
N72396      465 bp mRNA EST 02-APR-1996
LOCUS      N72396
DEFINITION YV39c11.r1 Soares fetal liver spleen INF5 Homo sapiens cDNA clone
            IMAGE:245108 5' similar to gb:xl6150_cds1 L-SELECTIN PRECURSOR
            (HUMAN);, mRNA sequence.
ACCESSION  N72396

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	VERSION	WT2396.1	GI:1229500
	KEYWORDS	EST.	
	SOURCE	human.	
	ORGANISM	Homo sapiens	
	Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria;	Primates; Catarrhini; Hominiidae; Homo.	
	REFERENCE	1 (bases 1 to 465)	
	AUTHORS	Hillier,L., Clark,N., Dubnau,T., Elliston,K., Hawkins,M., Holman M., Hultman,M., Kucsha,T., Le,M., Lennon,G., Marris,M., Parsons,J. Rifkin,L., Roiffinng,T., Soares,M., Tan,F., Trevaaskin,E., Waterston, R., Williamson,A., Wohldmann,P. and Wilson,R. The WashU-Merck EST Project Unpublished (1995) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNLN ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: reverse ER High quality sequence stop: 369.	
	TITLE	JOURNAL	
	COMMENT		
	FEATURES		
	Source	Location/Qualifiers	
	/organism="Homo sapiens"	.1..465	
	/db_xref="GDB:3794354"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:245108"		
	/clone.lib="Soares fetal liver spleen INFLS"		
	/sex="male"		
	/dev_stage="20 week-post conception fetus"		
	/lab_host="DH10B (ampicillin resistant)"		
	/note="Organ: Liver and Spleen; Vector: pTR3D (Pharmacia with a modified polylinker); Site.1: Pac I; Site.2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer[15' AACGGAGAAATTAATTAAAGAAGCTTTTTTTTTTTTTTTC 3'] , double-stranded cDNA was ligated to Eco RI adaptors (Pharmacial), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTR73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."		
OY	BASE COUNT	123 a 107 c 103 g 127 t	5 others
Dy	ORIGIN		
OY	Query Match	18.0%; Score 406.4; DB 159; Length 465;	
Best Local Similarity	97.6%;	Pred. No. 4.8e-104;	
Matches 454; Conservative	0; Mismatches 4;	Indels 7; Gaps 4;	
OY	709 TGATTCACGTGAGCGCTTGAGGCCCCAGAGCTGGTAGCACTGCATCACCCT	768	
Dd	4 TGAATTCAGTGAGCGCTTGAGGCCCCAGAGCTGGTAGCACTGCATCACCCT	768	
OY	769 TTGGAACCTCAGCTTCAGCTCACAGTGTGCTTCAGCTGCTGTGAAGAACAACTTAA	828	
Dd	62 TTGGAACCTCAGCTTCAGCTTCACAGTGTGCTTCAGCTGCTGTGAAGAACAACTTAA	120	
OY	829 CTGGGATGAGAAAACAACCCCTGTGACCATTTGGAAAACTGCTCATCTCAGAACCAACT	888	
Dd	121 CTTGGGATGAGAAAACAACCCCTGTGACCATTTGGAAAACTGCTCATCTCAGAACCAACT	180	
OY	889 GTCAAAGTATTCAGTGTGAGCGCTGTATCAGACACAGATTTGGGAGTCATGAAGACTAGCC	948	
Dd	181 GTCAAAGTATTCAGTGTGAGCGCTGTATCAGACACAGATTTGGGAGTCATGAAGACTAGCC	240	
OY	949 ATCCCCCTGGCCAGCTTCAGCTTTAAGCTTGATATA---CCCTCATCTGCTCAGAAAGGA	1004	
Dd	241 ATCCCCCTGGCCAGCTTCAGCTTTAAGCTTGATATA---CCCTCATCTGCTCAGAAAGGA	300	
OY	1005 ACTGAGTTAAATTTGGGAAGAAAACAATTTGTGANATCTGGAAATCTGGTCAAAATCCT	1064	
Dd	301 ACAGAGTTAAATTTGGGAAGAAAACAATTTGTGANATCTGGAAATCTGGTCAAAATCCT	360	

Qy	1065	AGCCCAATATGTGCAAAATTTGGCAAAAAGTTTCTCAATGATTAAGAGGCTAATTATAC	1124
Db	361	AGTCCAATATGTGCAAAATTTGGCAAAAAGTTTCTCAATGATTAAGAGGCTAATTATAC	420
Qy	1125	CCCCCTTCATTCACAGTGGCAGTCATGGTACTGCAATTCCTGGG	1169
Db	421	CCCCCTTCATTCACAGTGGCAGTCATGGTACTGCAATTCCTGGG	465
RESULT 12			
LOCUS	AV737434	552 bp	mRNA
DEFINITION	AV737434	CB Homo sapiens cDNA clone C8CECF10.5', mRNA sequence.	17-OCT-2000
ACCESSION	AV737434		
VERSION	AV737434.1	GI:10855015	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 552)		
TITLE	Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Chen,S., Mao,M. and Chen,Z.		
JOURNAL	Homo sapiens CB library cDNA clones		
COMMENT	Unpublished (2000)		
FEATURES	Source		
FEATURES	source		
BASE COUNT	166 a 120 c 149 g 112 t		
ORIGIN	166 a 120 c 149 g 112 t		
Query Match	17.8%; Score 403.2; DB 110; Length 552;		
Best Local Similarity	93.8%; Pred. No. 4.2e-103;		
Matches 496; Conservative	0; Mismatches 21; Indels 12; Gaps		
Qy	87	TCATGSGGCTGCGAAGAACTAGAAAGACCAACCAAGCCATGATTTCCATGGAAA	146
Db	15	TCGATGCGGCTGCGAAGACGACAGAAAGGCCCAACCAAGCCATGATTTCCATGGAAA	74
Qy	147	TGTGAGAGCACCCAGAGGGAGCTTATGAAACATCTTCAAGTTGGGGGTGGACAATGCTC	206
Db	75	TGTGAGAGCACCCAGAGGGAGCTTATGAAACATCTTCAAGTTGGGGGTGGACAATGCTC	134
Qy	207	TGTTTGATTTCTCGGCACATCATGGAACCTACTGCTGGAGTACCAATTTATCTGAAAAA	266
Db	135	TGTTTGATTTCTCGGCACATCATGGAACCTACTGCTGGAGTACCAATTTATCTGAAAAA	194
Qy	267	CCCATGAACTGGCAAAAGGCTGGAAGATTTCGCGAGACAAATTACACAGATTAGTTGGC	326
Db	195	CCCATGAACTGGCAAAAGGCTGGAAGATTTCGCGAGACAAATTACACAGATTAGTTGGC	254
Qy	327	ATACAAACAGAGCGGAAATTGATGTGAGAGAAGCTCTGCCCTTCAGTCTGTTTAC	386

Db	255	ATAC----	CAAGGGCGGAGANTGATATCTGGAGAAGACTCTGCCTTTCATTNGTTTC-TAC	309
OY	387	TACTGATAGGAATCCGGAAGATAGGAGAAATATGGACCTGGGTGGGAACAACAATCT		446
Db	310	TACTGGATPAGGAATCCGGAAGATAGGAGAAATATGGAC-TGGGTGGGAACAACAATCT		368
OY	447	CCTCCTGGAAGAAGCAGAGAACCTGGGGAGATGGTGAGGCCCAACAACAAGAAGAA-CAAGGA		505
Db	369	CTTACTGGAAGAAGCAGAGAACCTGGGGAGATGGTGAGGCCCAACAACAAGAAGAAACAAGGA		428
OY	506	GGAGCTGCGT-GGAGATCTTATCAAGAGAAAACAAGATCAGCAAATGGAAGCATGACG		564
Db	429	GGAGCTGCGTGGAGATCTTATCAAGAGAAAACAAGATCAGCAAATGGAAGCATGACG		488
OY	565	CCTGCCAACAACATAAAGCAGCCCTCTCTGTACACAGCTTCTTGCAACC		613
Db	489	CCTGCCAACAACATAAAGCAGCCCTCTCTGTACACAGCTTCTTGCAACC		533
RESULT_13				
LOCUS	AI434388/c			
DEFINITION	AI434388	478 bp	mRNA	EST 30-MAR-1999
	t148g06.x1	NCI_CGAP_Lym12	Homo sapiens cDNA clone IMAGE:2133754	3'
	similar to gb:X16150_cds1	L-SELECTIN PRECURSOR (HUMAN);		mRNA sequence.
ACCESSION	AI434388			
VERSION	AI434388.1	GI:4295831		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 478)			
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index			
JOURNAL	Unpublished (1997)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Life Technologies catalog #: 11547-015 DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLW at: www-bio.lnl.gov/dbip/image/image.html Insert Length: 1308 Std Error: 0.00 Seq primer: -40UP from Glibco High quality sequence stop: 378.			
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SOURCE	Location/Qualifiers			
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	/lab_host="DH10B"			
	/note="Organ: lymph node; Vector: PCMV-SPOrt6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"			
BASE COUNT	150 a 90 c 98 g 139 t			1 others
ORIGIN				
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Best Local Similarity	97.1%; Pred. No. 4.5e-103;			
Matches 431; Conservative	0; Mismatches 11; Indels 2; Gaps 2;			
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OY	1257	GGTGAAGAAATTTCTTGATACTTAAAAATCATGAGATCTTTAAATCTTTCATGAAA		1316

Db	364	GGTGAAGAAATTTCTTGGAACTACATAAAATCATGATGATCCCTTTAAATCCCTCCATGAA	325
OY	1317	CGTTTGTGTGTGGACCTCTACGTAAACATGAAAGTGTG-TTCCTTCAGTGCATCTT	1375
Db	324	CGTTTGTGTGTGGACCTCTACGTAAACATGAAAGTGTGTCNTTCAAGTGCATCTG	265
OY	1376	GGAAATTTCTACACCGACCAACAGTCTTCAAGCTTCATTTCCGCTCATTTATCCCT	1435
Db	264	GGAAATTTCTACACCGACCAACAGTCTTCAAGCTTCATTTCCGCTCATTTATCCCT	205
OY	1436	CAACCCCGACGCCACAGGTGTTTATACAGCTCAGCTTTTGTGCTTTCAGGAAACA	1495
Db	204	CAACCCCGACGCCACAGGTGTTTATACAGCTCAGCTTTTGTGCTTTCAGGAAACA	145
OY	1496	AATAAGACCAT-AAGGAAAGAGATTGATGGAATATTAAGATGGCTGACTTTGCTCTT	1554
Db	144	AATAAGACCATTAAGGAAAGAGATTGATGGAATATTAAGATGGCTGACTTTGCTCTT	85
OY	1555	CTTGACTCTGTTTTCAGTTTCATTCATTCAGTGTCTGACTTGTATGACAGCACTTTAAATG	1614
Db	84	CTTGACTCTGTTTTCAGTTTCATTCATTCAGTGTCTGACTTGTATGACAGCACTTTAAATG	25
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Db	24	AAGTGCAAATTTGATACATATGTG 1	
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DEFINITION	w45c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens CDNA clone		
ACCESSION	AI694304		
VERSION	AI694304.1	GI:4971644	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 566)		
AUTHORS	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	Unpublished (1997)		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
COMMENT	Email: cgaps-remail.nih.gov		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
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	Seq primer: -40UP from Glbco		
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	Equal amounts of plasmid DNA from three normalized		
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	vitro. Following HAP purification, this DNA was used as		
	tracer in a subtractive hybridization reaction. The driver		
	was PCR-amplified cDNAs from pools of 5,000 clones made		
	from the same 3 libraries. The pools consisted of		
	1.M.A.G.E. clones 297480-302087, 682632-687239,		
	726408-728711, and 729096-731399. Subtraction by Bento		
	Soares and M. Fatima Bonaldo.		
BASE COUNT	189 a 86 c 139 g 152 t		
ORIGIN			

Query Match 17.7%; Score 399.8; DB 23; Length 566;
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 ACCESSION BF902611
 VERSION BF902611.1 GI:12294070
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 403)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 Contact: Simpson A.J.J.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPERB/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=CMI6t2-CMI-MT0238-
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 ,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
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BASE COUNT 104 a 95 c 100 g 104 t
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Query Match 17.6%; Score 396.6; DB 171; Length 403;
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 Job time: 4520 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 12, 2001, 23:18:25 ; Search time 3951.8 Seconds
(without alignments)
8841.957 Million cell updates/sec

Title: US-09-119-209-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 3: gb_ba3:*
- 4: gb_in1:*
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- 9: gb_pat1:*
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- 96: gb_pr12:*
- 97: gb_pr13:*
- 98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2161	95.7	2354	97	HUMLNHR	M25280 Human lymph
4	2127.8	94.2	2323	93	HSLDEU8	X17519 Human mRNA
5	2087.6	92.4	2330	9	AR016679	AR016679 Sequence
6	2087.6	92.4	2330	9	AR040718	AR040718 Sequence
7	2087.6	92.4	2330	9	AR054061	AR054061 Sequence
8	2087.6	92.4	2330	10	I70140	I70140 Sequence 1

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9 2087.6 92.4 2330 93 HSLYAMI X16150 Human Lym-
10 1532.2 67.8 1569 93 HSA246000 A524600 Homo sapi
11 1351.2 59.8 1510 97 PHU52074 U52074 Papio hamad
12 1101.4 48.8 1119 97 PMU73728 PMU73728 Pan troglod
13 1085.5 48.0 1119 97 PMU73729 PMU73729 Pongo pygma
14 1056.6 46.8 1119 97 MMU73730 MMU73730 Macaca mula
15 1037 45.9 1680 7 OC026535 U26635 Oryctolagus
16 970.2 42.9 141589 92 HSL17P20 AL021940 Homo sapi
17 963.8 42.7 2650 7 BTLECAM1 X62882 B. taurus mr
18 950.8 42.1 1120 54 G06371 G06371 human STS W
19 922.2 40.8 1696 9 AR054070 AR040727 Sequence
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22 856.8 37.9 2199 94 M0SLHR M25324 Mouse perip
23 856.8 37.9 2214 94 AR060686 AR060686 Sequence
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25 827.8 36.6 1479 94 MMLNHR X14772 Mouse mRNA
26 820 36.3 1431 94 M0SLHRCA M36058 Mouse lymph
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28 794.4 35.2 1272 95 RATELCAM1 D10831 Rat mRNA fo
29 385.2 17.1 531 9 AR054064 AR054064 Sequence
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33 310 13.7 1833 10 A13650 A13650 Sequence 2
34 310 13.7 3834 9 AR110476 AR110476 Sequence
35 310 13.7 3834 97 HUMELAMA M24736 Human endot
36 310 13.7 3854 10 I43649 I43649 Sequence 1
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38 309 13.7 2703 7 BOVPS L12041 Bovine P-se
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ALIGNMENTS

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VERSION AR060685.1 GI:5987135
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2259)
AUTHORS Lasky, L.A., Rosen, S.D., Stachel, S.E. and Singer, M.S.
TITLE Soluble lymphocyte homing receptors
JOURNAL Patent: US 5840844-A 1 24-NOV-1998;
FEATURES
source 1..2259
location/Qualifiers
BASE COUNT 635 a 517 c 488 g 619 t
ORIGIN

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Query Match 100.0%; Score 2259; DB 9; Length 2259;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ACCESSION X16070.1
 VERSION X16070.1
 KEYWORDS lymphocyte adhesion receptor; lymphocyte homing receptor; transmembrane protein.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 2259)
 AUTHORS Bowen,B.R., Nguyen,T. and Lasky,L.A.
 TITLE Characterization of a human homologue of the murine peripheral lymph node homing receptor
 JOURNAL J Cell Biol. 109 (1), 421-427 (1989)
 MEDLINE 89308881
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 VERSION M25280.1 GI:187182
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2354)
 AUTHORS Siegelman, M. H. and Weissman, I. L.
 TITLE Human homologue of mouse lymph node homing receptor: evolutionary

conservation at tandem cell interaction domains
Proc. Natl. Acad. Sci. U.S.A. 86 (14), 5562-5566 (1989)

JOURNAL 89315637
MEDLINE
COMMENT Draft entry and computer-readable sequence for [1] kindly provided
by M.H.Stegelman, 02-JUN-1989.

FEATURES Location/Qualifiers

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QY	1244	TTAAATGCCCCCTGTGGTGAAGAAAATTTCTTGGATATCTAAAAATCATGAGATCTTTTAAA	1303
Db	1204	TTAAATGCCCCCTGTGGTGAAGAAAATTTCTTGGATATCTAAAAATCATGAGATCTTTTAAA	1263
QY	1304	TCCCTTCATGAAAGCTTTTGTGTGTGGGCACTCCCTACGTCAAACATGAAAGTGTG-TTCC	1363
Db	1264	TCCCTTCATGAAAGCTTTTGTGTGTGGGCACTCCCTACGTCAAACATGAAAGTGTGTTC	1323
QY	1363	TTACGTCATCTGGGAGAGATTTTACCCGACCAACAGTTCTTTCAAGCTCCATTTCCGCC	1423
Db	1324	TTACGTCATCTGGGAGAGATTTTACCCGACCAACAGTTCTTTCAAGCTCCATTTCCGCC	1383
QY	1423	CTCATTTATCCCTCAACCCCCAGCCCAAGGCTTTATACGCTCAGCTTTTGTGCTTTT	1483
Db	1384	CTCATTTATCCCTCAACCCCCAGCCCAAGGCTTTATACGCTCAGCTTTTGTGCTTTT	1443
QY	1483	CTGAGGAGAAACAAATTAAGACCAT-TAAGGAAAGATTCATGTGGAATTAAGAGATGGCT	1543
Db	1444	CTGAGGAGAAACAAATTAAGACCATTAAGGAAAGATTCATGTGGAATTAAGAGATGGCT	1503
QY	1542	GACCTTGTGCTCTTCTTGACACTCTTGTGTTTTCAGTTTCATTCAGTGTCTGTACTTGATGACAG	1603
Db	1504	GACCTTGTGCTCTTCTTGACACTCTTGTGTTTTCAGTTTCATTCAGTGTCTGTACTTGATGACAG	1563
QY	1602	ACACTTCCTAAATGAAAGGCAAAATTTGTATCATATTTGGAATATGAGACTCAGTTTCTTGCA	1663
Db	1564	ACACTTCCTAAATGAAAGGCAAAATTTGTATCATATTTGGAATATGAGACTCAGTTTCTTGCA	1623
QY	1662	GATCAAAATTCACGTGCTCTTCTGTATCTGTGGAGGATCACTCTTATATGAAGATTTCAA	1723
Db	1624	GATCAAAATTCACGTGCTCTTCTGTATCTGTGGAGGATCACTCTTATATGAAGATTTCAA	1683

QY	1722	AGTGTACGCTCCCTTTCTTTCTTAACACACGAAAGTAATGGGGTCGCTCAAGTTGA	1781
QY	1722	AGTGTACGCTCCCTTTCTTTCTTAACACACGAAAGTAATGGGGTCGCTCAAGTTGA	1781
Db	1684	AGGTGTACGCTCCCTTTCTTTCTTAACACACGAAAGTAATGGGGTCGCTCAAGTTGA	1743
QY	1782	AAGAGTCCATTTGGACATGTACCTCGCGCTGTGGAATTTGACCATCTCATTTTAACGTG	1841
Db	1744	AAGAGTCCATTTGGACATGTACCTCGCGCTGTGGAATTTGACCATCTCATTTTAACGTG	1803
QY	1842	CTTACGAGCCCTCCCAACCTTTCTTACGACACACCTCTTTTTCAGTTGGCTGACTTCCACACC	1901
Db	1804	CTTCA - GCCCTCCCAACCTTTCTTACGACACACCTCTTTTTCAGTTGGCTGACTTCCACACC	1862
QY	1902	TAGCATCTCATGTAGTGGCCAGCAAGAAAAGGAGAGAAGAGAATAATAGCTCGCGGTTTTT	1961
Db	1863	TAGCATCTCATGTAGTGGCCAGCAAGAAAAGGAGAGAAGAGAATAATAGCTCGCGGTTTTT	1922
QY	1962	AGTTTGGGGGCTTTTCTGTCTTTCTTTTATGAGACCCATTCATATTTCTATATGTCAATGT	2021
Db	1923	AGTTTGGGGGCTTTTCTGTCTTTCTTTTATGAGACCCATTCATATTTCTATATGTCAATGT	1982
QY	2022	TTCTTTTATCACGATATTTATTTAGTAAGAAMAACATCACTGMAATGCTAGCTGCAAGTGACA	2081
Db	1983	TTCTTTTATCACGATATTTATTTAGTAAGAAMAACATCACTGMAATGCTAGCTGCAAGTGACA	2042
QY	2082	TCTCTTTGATGTGCATATGGAAGAGTTAAACAGGTGGAGAAATTCCTTGATTTACAAATGA	2141
Db	2043	TCTCTTTGATGTGCATATGGAAGAGTTAAACAGGTGGAGAAATTCCTTGATTTACAAATGA	2102
QY	2142	AATGCTCTCTTTTCCCTCGCCCGCCAGAACCTTTTATCC - ACTTACCTAGATTTCTACATATT	2200
Db	2103	AATGCTCTCTTTTCCCTCGCCCGCCAGAACCTTTTATCCGACTTACCTAGATTTCTACATATT	2162
QY	2201	CTTTAAATTTCAATCTCAGGCGCTCCGTCACACCCAC	2235
Db	2163	CTTTAAATTTCAATCTCAGGCGCTCCCTCAGACCCAC	2197
RESULT	5		
AR016679			
LOCUS	AR016679	2330 bp	DNA
DEFINITION	Sequence 1 from patent US 5776775.		PAT
ACCESSION	AR016679		05-DEC-1998
VERSION	AR016679.1	GI:3972956	
KEYWORDS			
SOURCE			
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2330)		
TITLE	Tedder,T.F. and Sperltini,O.G.		
JOURNAL	Anti-LAM 1-3 antibody and hybridoma		
FEATURES	Patent: US 5776775-A 1 07-JUL-1998;		
	Location/Qualifiers		
	1..2330		
	Source		
	1..2330		
BASE COUNT	661 a	522 c	487 g
ORIGIN		660 t	
Query Match	92.4%;	Score 2087.6;	DB 9;
Best Local Similarity	98.5%;	Pred. No. 0;	Length 2330;
Matches 2161;	Conservative 0;	Mismatches 24;	Indels 9;
		Gaps 5;	
QY	44	CCCTTTGGCAAGGACCTGACACCCCTTGGCTAATGCAAGAGGCTCAATGGGCTGGAGAG	103
Db	7	CCCTTTGGCAAGGACCTGACACCCCTTGGCTAATGCAAGAGGCTCAATGGGCTGGAGAG	66
QY	104	AACGTAGAAGAGCAACAAAGCCATGATATTTTCATGGAATGTCAAGACACCCAGAG	163
Db	67	AACGTAGAAGAGCAACAAAGCCATGATATTTTCATGGAATGTCAAGACACCCAGAG	126
QY	164	GGACTTATGGAACATCTTCAAGTGTGGGGGTGACACATGCTCTGTGTGATTTCTGTGC	223
Db	127	GGACTTATGGAACATCTTCAAGTGTGGGGGTGACACATGCTCTGTGTGATTTCTGTGC	186

QY	224	ACATCATGSAACCTTACTGCTGGACCTTACCATTAATTCGAAAAACCCATGAACTGGCAAG	283
Db	187	ACATCATGSAACCGACTGCTGGACCTTACCATTAATTCGAAAAACCCATGAACTGGCAAG	246
QY	284	GGGTACAAGATTCTGCCGAGCAATTACACGATTTTGTTGCCCTACAAAAACAAGCGGA	343
Db	247	GGGTACAAGATTCTGCCGAGCAATTACACGATTTTGTTGCCCTACAAAAACAAGCGGA	306
QY	344	AATTAGTATCTGGAGAAGACTCTGCCCTTCAGTCGTTCTTACTACTAGATAGAAATCCG	403
Db	307	AATTAGTATCTGGAGAAGACTCTGCCCTTCAGTCGTTCTTACTACTAGATAGAAATCCG	366
QY	404	GAAAGATAGAGAAATATGAGAGCTGGGTGGAAACCAACAATCTCTCACTAGAGAAGCAGA	463
Db	367	GAAAGATAGAGAAATATGAGAGCTGGGTGGAAACCAACAATCTCTCACTAGAGAAGCAGA	426
QY	464	GAAGTGGGAGATGGTGGAGCCCAACANACAAGAACAGAGACTGCGCTGGAGATCTA	523
Db	427	GAAGTGGGAGATGGTGGAGCCCAACANACAAGAACAGAGACTGCGCTGGAGATCTA	486
QY	524	TATCAAGAAAAACAAGATGCAAGGCAAATGGAAAGATGAGAGCCGTGCACAAATAAAGC	583
Db	487	TATCAAGAAAAACAAGATGCAAGGCAAATGGAAAGATGAGAGCCGTGCACAAATAAAGC	546
QY	584	AACCCCTGTGTACACAGCTTCTTGCCACGCCCTGGTCAATGCAATGGCCATGAGAAATGTGT	643
Db	547	AACCCCTGTGTACACAGCTTCTTGCCACGCCCTGGTCAATGCAATGGCCATGAGAAATGTGT	606
QY	644	AGAATATCATTAATATACACCTGCAACTGATGATGGGGTACTATGAGGCCGCCAGTGTCA	703
Db	607	AGAATATCATTAATTAATACACCTGCAACTGATGATGGGGTACTATGAGGCCGCCAGTGTCA	666
QY	704	GCTTGTGATTCAGTGTGAGCCTTTGGAGGCCCAAGAGCTGGTACCATGGAGTGTACTCA	763
Db	667	GTTTGTGATTCAGTGTGAGCCTTTGGAGGCCCAAGAGCTGGTACCATGGAGTGTACTCA	726
QY	764	CCCCCTTGGAAACTTCAGCTTCAGCTCAACAGTGTGCTTCAGCTGCTGTGAAGAACAA	823
Db	727	CCCCCTTGGAAACTTCAGCTTCAGCTTCAGCTTCAGCTGCTGTGAAGAACAA	786
QY	824	CTTAATCTGGAAATGGAAGAACACCTGTGACACATTTGGAAACTGGTCAATCTCCAGAAC	883
Db	787	CTTAATCTGGAAATGGAAGAACACCTGTGACACATTTGGAAACTGGTCAATCTCCAGAAC	846
QY	884	AACCTGTCAAGTGAATCAGTGTGAGCCTCATAGCACCAGATTTGGGGATCATATGAATCG	943
Db	847	AACCTGTCAAGTGAATCAGTGTGAGCCTCATATAGCACCAGATTTGGGGATCATATGAATCG	906
QY	944	TAGCCATCCCTGGCCAGACTTCAGCTTACCTGTGCATGTACCTTCATCTGCTCAGAAG	1003
Db	907	TAGCCATCCCTGGCCAGACTTCAGCTTACCTGTGCATGTACCTTCATCTGCTCAGAAG	966
QY	1004	AACGAGTAAATTTGGGAAGAAAGAAACCATTTGTGAATATCTGGAATGTGGTCAAAATCC	1066
Db	967	AACGAGTAAATTTGGGAAGAAAGAAACCATTTGTGAATATCTGGAATGTGGTCAAAATCC	1026
QY	1064	TAGTCCATATGTCAAAAAATTTGGCAAAAGTTCTCAATGATTAAGAGAGGGGATTAATA	1123
Db	1027	TAGTCCATATGTCAAAAAATTTGGCAAAAGTTCTCAATGATTAAGAGAGGGGATTAATA	1086
QY	1124	CCCCCTTCAATTCAGAGTGGCAGTCAATGGTTACTGCATCTCTGGGTGGCAATTAATCAT	1183
Db	1087	CCCCCTTCAATTCAGAGTGGCAGTCAATGGTTACTGCATCTCTGGGTGGCAATTAATCAT	1146
QY	1184	TTGGCTGTGCAAGAGATTTAAAAAAGCAAGAAATCCAAGACAGATATGATGACCCATA	1243
Db	1147	TTGGCTGTGCAAGAGATTTAAAAAAGCAAGAAATCCAAGACAGATATGATGACCCATA	1206
QY	1244	TTTAATGTGCCCTGTGGTGAAGAAATTTCTGGAAATCTTAAAAATATAGATCCTTTAAA	1303
Db	1207	TTTAATGTGCCCTGTGGTGAAGAAATTTCTGGAAATCTTAAAAATATAGATCCTTTAAA	1266

QY	1304	TCCTTCCATGAAGACCTTTTGTGTGTGTGGCACCTCTCTACGTCAAAACATGAAGTGTG--TTCC	1362
Db	1267	TCCTTCCATGAAGACCTTTTGTGTGTGTGGCACCTCTCTACGTCAAAACATGAAGTGTGTTC	1326
QY	1363	TTTCAGTGCATCTGGGAGAATTTCTACCGGACCAACAGTTCTTCACCTCCATTTGCGGCC	1422
Db	1327	TTTCAGTGCATCTGGGAGAATTTCTACCTGACCAACAGTTCTTCACCTTCCATTTCAACC	1386
QY	1423	CTCAATTTATCCCTCAACCCCGACGCGCAGAGTGTATACAGCTCAGCTTTTGTCTTTT	1482
Db	1387	CTCAATTTATCCCTCAACCCCGACGCGCAGAGTGTATACAGCTCAGCTTTTGTCTTTT	1446
QY	1483	CTGAGAGAAACAAATTAAGACCAT--AAGGAAAGGATTCATGTGGAAATTAAGATGCGCT	1541
Db	1447	CTGAGAGAAACAAATTAAGACCAATAAGGAAAGGAAAGGATTCATGTGGAAATTAAGATGCGCT	1506
QY	1542	GACTTGTGCTTTCTTGACCTCTTCTTTTTCAGTTCAATTCAGTGCAGTACTGATGACAG	1601
Db	1507	GACTTGTGCTTTCTTGACCTCTTCTTTTTCAGTTCAATTCAGTGCAGTACTGATGACAG	1566
QY	1602	ACACTTCTTAAATGAAGTGCAAATTTGATACATATGTGAATATGAACTCAGTTTCTTTGCA	1661
Db	1567	ACACTTCTTAAATGAAGTGCAAATTTGATACATATGTGAATATGAACTCAGTTTCTTTGCA	1626
QY	1662	GATCAAAATTTCAACGCGCTCTTGATACCTGTGGAGAGTACACTCTTATAGAAAGTTCAA	1721
Db	1627	GATCAAAATTTGCGCTGCTCTTGATAC--GTGAGAGTACACTCT---ATGAGTCAA	1680
QY	1722	AAGTCTACGCTCTCTTTCTTTCTTAACTCCAGTGAAGTATGAGGGTCTCGTCAAGTTGA	1781
Db	1681	AAGTCTACGCTCTCTTTCTTTCTTAACTCCAGTGAAGTATGAGGGTCTCGTCAAGTTGA	1740
QY	1782	AAGAGTCTAATTGCACTGTAGCCCTGCGCTGTGTAATTGGACATCCATTTAACTGG	1841
Db	1741	AAGAGTCTAATTGCACTGTAGCCCTGCGCTGTGTAATTGGACATCCATTTAACTGG	1800
QY	1842	CTTCAAGCTCCCGACCTCTTGTAGCCACTCTCTTTTCAATGTGGCTGTCCACATCC	1901
Db	1801	CTTCA--GCTGCTCCCACTCTTGTAGCCACTCTCTTTTCAATGTGGCTGTCCACATCC	1859
QY	1902	TAGCATCTCATGATGTGCCAAGCAAAAGAGAGAGAAGAAATACCTGCGCGGTTTTT	1961
Db	1860	TAGCATCTCATGATGTGCCAAGCAAAAGAGAGAGAAGAAATACCTGCGCGGTTTTT	1919
QY	1962	AGTTTGGGGGTTTGTCTTCTTTTATGAGACCATTTCTAATTTCTTATATGCAATGT	2021
Db	1920	AGTTTGGGGGTTTGTCTTCTTTTATGAGACCATTTCTAATTTCTTATATGCAATGT	1979
QY	2022	TTCTTTTATACCAATATATTATAGTAAAGAAACATACATGAAATGTGTAGCTGCAAGTACA	2081
Db	1980	TTCTTTTATACCAATATATTATAGTAAAGAAACATACATGAAATGTGTAGCTGCAAGTACA	2039
QY	2082	TTCTTTTATGATGTATATGAAAGGTTAAACAGGTGGAGAAATTCCTTGATTCACAATGA	2141
Db	2040	TTCTTTTATGATGTATATGAAAGGTTAAACAGGTGGAGAAATTCCTTGATTCACAATGA	2099
QY	2142	AATGCTCTCTTTCCCTGTGCGCCAGAACCTTTTATCCACTTACCTAGATTTCTACATATTC	2201
Db	2100	AATGCTCTCTCTTTCCCTGTGCGCCAGAACCTTTTATCCACTTACCTAGATTTCTACATATTC	2159
QY	2202	TTTAAATTTATCTGACGGCTCTCTTCAACCCGAC	2235
Db	2160	TTTAAATTTATCTGACGGCTCTCTTCAACCCGAC	2193

[illegible]

D	367	GAAAGTATAGAGAAATATATGACGTGGGTGGAAACCAAAATCTCTCACTGAAAGACGA	426
Q	464	GAACGTGGGAANTGATGAGCCCAACAACAAGAAAGAGAGACTGCTGGAGATCTA	523
D	427	GAACGTGGGAGATGCTGAGCCCAACAACAAGAAAGAGAGACTGCTGGAGATCTA	466
Q	524	TATCAAGGAACAAAGATCTAGGCAATATGAAAGTACGCTTGCCCAAACTPAAAGC	583
D	487	TATCAAGGAACAAAGATCTAGGCAATATGAAAGTACGCTTGCCCAAACTPAAAGC	546
Q	584	AGCCCTGTGTACACAGCTCTTGCCAGCCCTGGTATGACAGTGGCCATGGAGAAATGTG	643
D	547	AGCCCTGTGTACACAGCTCTTGCCAGCCCTGGTATGACAGTGGCCATGGAGAAATGTG	606
Q	644	AGAAATATCAATATATCACCCTGCAACTGTGATGTGGGTACTATGTGGGCCCAAGTGTCA	703
D	607	AGAAATATCAATATATATACCTGCACACTGTATGTGGGTACTATGTGGGCCCAAGTGTCA	666
Q	704	GCTTGATTCAGTGTGAGCCCTTGGAGGCCCCAGAGTGGGTACCTGACCTGTACTCA	763
D	667	GTTTGATTCAGTGTGAGCCCTTGGAGGCCCCAGAGTGGGTACTATGTGGGCCCAAGTGTCA	726
Q	764	CCCCCTTGGAACTTCAGCTTACGCTCAAGTGTGACCTTGACGCTGCTCAAGACAA	823
D	727	CCCCCTTGGAACTTCAGCTTACGCTCAAGTGTGACCTTGACGCTGCTCAAGACAA	786
Q	824	CTTAACTGGATTTGAAGAAACCACTGTGACCACTTTGGAACTGTGATCTTCAGAAC	883
D	787	CTTAACTGGATTTGAAGAAACCACTGTGACCACTTTGGAACTGTGATCTTCAGAAC	846
Q	884	AACCTGTCAAGTATTCAGTGTGAGCCCTTTCAGACCAAGTTTGGGATCATAGAACG	943
D	847	AACCTGTCAAGTATTCAGTGTGAGCCCTTTCAGACCAAGTTTGGGATCATAGAACG	906
Q	944	TACCACTCCCTGGCCAGCTTACGCTTACCTGTGATGTACCTTCATCTGCTCAGAAAG	1003
D	907	TACCACTCCCTGGCCAGCTTACGCTTACCTGTGATGTACCTTCATCTGCTCAGAAAG	966
Q	1004	AACGTGTTAAATTTGGGAAGAAAGAAACCAATTTGGATATCTGGAATCTGTCAAATCC	1063
D	967	AACGTGTTAAATTTGGGAAGAAAGAAACCAATTTGGATATCTGGAATCTGTCAAATCC	1026
Q	1064	TAGTCCAAATATGTCAAAATTTGGACAAAGTTTCTCAATGATTAAGAGAGGATTAATA	1123
D	1027	TAGTCCAAATATGTCAAAATTTGGACAAAGTTTCTCAATGATTAAGAGAGGATTAATA	1086
Q	1124	CCCCCTTCATTCACAGTGGGACATGTTACTGCAATCTCTGGGTGGCATTTATCAT	1183
D	1087	CCCCCTTCATTCACAGTGGGACATGTTACTGCAATCTCTGGGTGGCATTTATCAT	1146
Q	1184	TGCGCTGGCAAGAGATTTAAAAAAGGCAAGAAATCCAGAGAAATATGAAATGACCATTA	1243
D	1147	TGCGCTGGCAAGAGATTTAAAAAAGGCAAGAAATCCAGAGAAATATGAAATGACCATTA	1206
Q	1244	TTAAATGCCCTTGTGTGAAGAAATTTCTTGGAAATCTAAAAATCATGAGATCTCTTAAA	1303
D	1207	TTAAATGCCCTTGTGTGAAGAAATTTCTTGGAAATCTAAAAATCATGAGATCTCTTAAA	1266
Q	1304	TCTCTCCATGAAAGTTTGTGTGTGGGACACCTCGACGTCAAAATGAAATGTGG-TTCC	1362
D	1267	TCTCTCCATGAAAGTTTGTGTGTGGGACACCTCGACGTCAAAATGAAATGTGTGTTCC	1326
Q	1363	TTTCACTGATCTGGGAGATTTTACCCGACCAACAGTTCTCTGACGTTCCATTTGGCC	1422
D	1327	TTTCACTGATCTGGGAGATTTTACCTGACCAACAGTTCTCTGACGTTCTCAATTTACCC	1386
Q	1423	CTCAATTTATGCTTCAACCCCAACCCACAGGTGTTATACAGCTCAGCTTTTGTCTTTT	1482
D	1387	CTCAATTTATGCTTCAACCCCAACCCACAGGTGTTATACAGCTCAGCTTTTGTCTTTT	1446
Q	1483	CTGAGGAAACAAATTAAGACAT-AAAGGAAGATTCATGTGAAATTAAGAGAGGCT	1541
D	1447	CTGAGGAAACAAATTAAGACATTAAGGAAGATTCATGTGAAATTAAGAGAGGCT	1506

OY	1542	GACITTTGCTCTTTCCTTRACACTCTGTTTTGAGITTTCAATTCAATGACTGCTGTAACCTTGATGACAG	1601
Db	1507	GACITTTGCTCTTTCCTTRACACTCTGTTTTGAGITTTCAATTCAATGACTGCTGTAACCTTGATGACAG	1566
OY	1602	ACACTTCCMAATGAAGTAGCAAAATTTAATACATATGGAATATGAGCTAGTCAAGTTTTCTTGCA	1661
Db	1567	ACACTTCCMAATGAAGTAGCAAAATTTAATACATATGGAATATGAGCTAGTCAAGTTTTCTTGCA	1626
OY	1662	GATCAAAATTTGACGTGCTCTTTCGTATCTACTGTGGAGGTACACTCTTATAAGAAATTCAAA	1721
Db	1627	GATCAAAATTTGCGCTCCTCTTCGTATAC -GTGGAGGTACACTCT- --- ATAGAAGTCAA	1680
OY	1722	AAGCTACGCGTCCCTTTCCTTTCCTAACCTCAGGAAGTAAATGGGCGCGCTCAAGTTGA	1781
Db	1681	AAGCTACGCGTCTCTCTTCTTCTTACTCCAGTGAAGTAAATGGGCTCTGCTCAAGTTGA	1740
OY	1782	AAGAGTCCCATTTTGCACTGTAGCCTGCGCTGTGTAATTTGAGACATCCATTTAACTGG	1841
Db	1741	AAGAGTCCCATTTTGCACTGTAGCCTGCGCTGTGTAATTTGAGACATCCATTTAACTGG	1800
OY	1842	CTTGAGGCGTCCCACCTCTTCTTGAGCACCTCCTTTTCAGTTGGCGACTCCACACGC	1901
Db	1801	CTTCA -GCTTCCACCTTCTTCAGCCACCTCTCTTTTCAFTGGCTGACTCCACACGC	1859
OY	1902	TAGCATCTCATGAGTGTGCCAAGAAAAAGAGAGAGAAATAGCCTGCGCGGTTTTT	1961
Db	1860	TAGCATCTCATGAGTGTGCCAAGAAAAAGAGAGAGAAATAGCCTGCGCGGTTTTT	1919
OY	1962	AGTTTGGGGGTTTTGCTGTTTTCTTTTATGAGACCATTCCATTTCTTATATAGTAATGT	2021
Db	1920	AGTTTGGGGGTTTTGCTGTTTTCTTTTATGAGACCATTCCATTTCTTATATAGTAATGT	1979
OY	2022	TTCTTTTATCAGATATATTATTAGTAGAAACAATCACTGAATATGCTAGCTGCAGTGA	2081
Db	1980	TTCTTTTATCAGATATATTATTAGTAGAAACAATCACTGAATATGCTAGCTGCAGTGA	2039
OY	2082	TCCTCTTGAATGTCAATATGGAAGATTAAAAAGATGGAGAAATTCCTTGATTCACATGA	2141
Db	2040	TCCTCTTGAATGTCAATATGGAAGATTAAAAAGATGGAGAAATTCCTTGATTCACAAAGA	2099
OY	2142	AATGCTGCTCTTTCCTCCGTGCCCAAGAACTTTTATCACTATCAATATGATATATTC	2201
Db	2100	AATGCTGCTCTTTCCTCCGTGCCCAAGAACTTTTATCACTATCAATATGATATATTC	2159
OY	2202	TTTAAATTTCACTGACGAGCTCCCTCAACCCAC	2235
Db	2160	TTTAAATTTCACTGACGAGCTCCCTCAACCCAC	2193

RESULT	8								
LOCUS	170140	2330 bp	DNA						02-APR-1998
DEFINITION	Sequence 1 from patent US 5679346.								
ACCESSION	170140								
VERSION	170140.1	GI:3006275							
KEYWORDS	.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	Unclassified.								
AUTHORS	1 (bases 1 to 2330)								
TITLE	Teder,T.F. and Spettini,O.G.								
JOURNAL	Methods of blocking adhesion with anti-Iam1-3 antibody								
FEATURES	Patent: US 5679346-A 1 21-OCT-1997;								
source	Location/Qualifiers								
	1..2330								
BASE COUNT	/organism="unknown"								
ORIGIN	661 a	522 c	487 g	660 t					
Query Match	92.4%	Score 2087.6;	DB 10;	Length 2330;					
Best Local Similarity	98.5%;	Pred. NO. 0;							

	Matches	2161:	Conservative	0:	Mismatches	24:	Indels	9:	Gaps	5:
OY	44	CCCTTTGGCAAGAGACCTTGAGACCTTGTGCTAAGTCAAGAGAGCTCTCAATGGCTGCAGAA	103							
Db	7	CCCTTTGGGCAAGAGACCTTGAGACCTTGTGCTAAGTCAAGAGAGCTCTCAATGGCTGCAGAA	66							
OY	104	AACCTAGAGAGGACCAAGCAAAAGCCATGATATTTCCATGGAATGTCAAGAGCACCAGAG	163							
Db	67	AACCTAGAGAGGACCAAGCAAAAGCCATGATATTTCCATGGAATGTCAAGAGCACCAGAG	126							
OY	164	GGACCTTATGGAACATCTTTCANAGTTGTGGGGGGTGGACAAATGGCTGTGTGATTTCTGGC	223							
Db	127	GGACCTTATGGAACATCTTTCANAGTTGTGGGGGGTGGACAAATGGCTGTGTGATTTCTGGC	186							
OY	224	ACATATATGGAACCTACTGCTGACTTACCATTATTTCTGAAAAAACCCATGAACTGGCAAG	283							
Db	187	ACATCATGGAACCCGACACTGCTGACTTACCATTATTTCTGAAAAAACCCATGAACTGGCAAG	246							
OY	284	GGCTAGAAAGATTCTGCCGAGACATTTACACAGATTTTACTTGCCATACAAAACAGGGCGA	343							
Db	247	GGCTAGAAAGATTCTGCCGAGACATTTACACAGATTTTACTTGCCATACAAAACAGGGCGA	306							
OY	344	AATTAGATATCTGGGAAGAGACCTGCTCCCTTCACAGTGTCTTACTCTGTGGATAGGAATCG	403							
Db	307	AATTAGATATCTGGGAAGAGACCTGCTCCCTTCACAGTGTCTTACTCTGTGGATAGGAATCG	366							
OY	404	GAAAGATAGAGAGAAATATGGACGTGGGTGGGAACCAAAATCTCTCAGTGAAGAAGACAGA	463							
Db	367	GAAAGATAGAGAGAAATATGGACGTGGGTGGGAACCAAAATCTCTCAGTGAAGAAGACAGA	426							
OY	464	GAACTGGGGAGATGCTGAGCCCAACAGACAGAAGAACAAGAGAGACTCGTGGAGATCTA	523							
Db	427	GAACTGGGGAGATGCTGAGCCCAACAGACAGAAGAACAAGAGAGACTCGTGGAGATCTA	486							
OY	524	TATCAAGAAGAAACAAGAAATGCGAGCAATGGACATACCGCTGCCCAAAACTAAAGC	583							
Db	487	TATCAAGAAGAAACAAGAAATGCGAGCAATGGACATACCGCTGCCCAAAACTAAAGC	546							
OY	584	AGCCCTCTGTTTCAACAGGTTCTTGGCAGCCCGTGTATGACAGTGGCCATGGAATGTGT	643							
Db	547	AGCCCTCTGTTTCAACAGGTTCTTGGCAGCCCGTGTATGACAGTGGCCATGGAATGTGT	606							
OY	644	AGAAATCATCAATTAATTCACACACCTGCAACCTGTGATGTGGGGTACTATGSGGCCCACTGTCA	703							
Db	607	AGAAATCATCAATTAATTCACACACCTGCAACCTGTGATGTGGGGTACTATGSGGCCCACTGTCA	666							
OY	704	GCTTGTGATTCAGTGTGAGACCTTGTGGAGGCCCAACAGCTGGGTACCATGAGACTGTACTCA	763							
Db	667	GTTTGTGATTCAGTGTGAGACCTTGTGGAGGCCCAACAGCTGGGTACCATGAGACTGTACTCA	726							
OY	764	CCCTTTTGGAAACCTTCAGCTTCAGTCCACAGTGTCCCTTCAGCTGCTGTGAAGAAACAA	823							
Db	727	CCCTTTTGGAAACCTTCAGCTTCAGTCCACAGTGTCCCTTCAGCTGCTGTGAAGAAACAA	786							
OY	824	CTTAACTGGGATTTGGAAGAAACACCTGTGGAACATTTGGAAAACCTGTGATCTCCAGAAC	883							
Db	787	CTTAACTGGGATTTGGAAGAAACACCTGTGGAACATTTGGAAAACCTGTGATCTCCAGAAC	846							
OY	884	AACCTGTCAAGTGAATTCAGTGTGAGCCCTGTATCAGACACCAGATTTTGGGATCATCTACTG	943							
Db	847	AACCTGTCAAGTGAATTCAGTGTGAGCCCTGTATCAGACACCAGATTTTGGGATCATCTACTG	906							
OY	944	TAGGCATCCCCGGGCGAGCTTCAGGTTTACCTTCACATGTACCTTCATCTGCTCGAAGG	1003							
Db	907	TAGGCATCCCCGGGCGAGCTTCAGGTTTACCTTCACATGTACCTTCATCTGCTCGAAGG	966							
OY	1004	AACCTAGTTAATTTGGGAAGAAAGAAACCATTTGTGAATCATCTGGAAATCTGGTCAAACTC	1063							
Db	967	AACCTAGTTAATTTGGGAAGAAAGAAACCATTTGTGAATCATCTGGAAATCTGGTCAAACTC	1026							
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Db	1267	TCCTTCATGAAAGTTTTGTGTGGTGGACCTCTACGTCAACATGAAGTGTGTTC	1326
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DEFINITION	Human Lyam-1 mRNA for leukocyte adhesion molecule-1.	PRI	22-MAR-1995
ACCESSION	X16150		
VERSION	X16150.1	GI:34428	
KEYWORDS	cell surface protein; leukocyte adhesion protein; transmembrane protein.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthelia; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 2330)		
TITLE	Tedder,T.F.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (09-NOV-1989) Tedder T.F		
AUTHORS	2 (bases 1 to 2330) Tedder T.F		
	Disteche,C.M.		
	Isolation and chromosomal localization of cDNAs encoding a novel human lymphocyte cell surface molecule, LAM-1. Homology with the mouse lymphocyte homing receptor and other human adhesion proteins J. Exp. Med. 170 (1), 123-133 (1989)		
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Best Local Similarity	98.5%;	Freq. No. 0;	
Matches 2161; Conservative	0;	Mismatches 24;	Indels 9; Gaps 5;
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Db 67 AACTAGAGAAGACCAAGCAAGCATGATATTTTCATGGAATGTGAGACACCAGAG 126
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RESULT 10
HSA246000
LOCUS HSA246000 1569 bp mRNA PRI 08-SEP-1999

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DEFINITION Homo sapiens mRNA for leucocyte adhesion receptor, L-selectin.
ACCESSION AJ246000
VERSION AJ246000.1 GI:5852071
KEYWORDS L-selectin gene; leucocyte adhesion receptor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1569)
AUTHORS Fieger,C.B.
JOURNAL Thesis (1998) Freie Universitaet Berlin, Fachbereich Chemie
REFERENCE 2 (bases 1 to 1569)
AUTHORS Fieger,C.B.
TITLE Direct Submission
JOURNAL Submitted (04-SEP-1999) Fieger C.B., Benjamin Franklin Klinikum der
Freien Universitaet Berlin, Institut fuer Klinische Chemie &
Pathobiochemie, Hinderburgdamm 50, 12200 Berlin, GERMANY
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ACCESSION	U52074		
VERSION	U52074.1	GI:1326148	
KEYWORDS	olive baboon.		
SOURCE	Papio cynocephalus anubis		
ORGANISM	Eukaryota; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Papio.		
REFERENCE	1 (bases 1 to 1510)		
AUTHORS	Tsurushita, N., Fu, H. and Berg, E. L.		
JOURNAL	PCR cloning of the cDNA encoding baboon L-selectin		
MEDLINE	Gene 181 (1-2), 219-220 (1996)		
REFERENCE	2 (bases 1 to 1510)		
AUTHORS	Tsurushita, N.		
JOURNAL	Direct Submission		
TITLE	Submitted (21-MAR-1996) Nooya Tsurushita, Protein Design Labs, Inc., 2375 Garcia Avenue, Mountain View, CA 94043, USA		
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DEFINITION	Pan troglodytes L-selectin mRNA, complete cds.
ACCESSION	U73728
VERSION	U73728.1 GI:1656019
	05-NOV-1996

SOURCE ORGANISM

REFERENCE	1 (bases 1 to 1119)
AUTHORS	Budman, J. I., Fu, H., Johnson, C. E., Thakur, A. B., Berg, F. L., and

JOURNAL unpublished
REFERENCE 2 (bases 1 to 119)

TITLE Direct Submission
JOURNAL Submitted (08-OCT-1996) Protein Design Labs, Inc., 2375 Garcia Avenue, Mountain View, CA 94043, USA

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Db		1081	GGCAAGAAATCCAGAGAGATGATGAATGACCATTAATTAA	1119
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DEFINITION		Macaca mulatta L-selectin mRNA, complete cds.		
VERSION		U73730		
KEYWORDS		U73730.1 GI:1658015		
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ORGANISM		rhesus monkey.		
REFERENCE		Macaca mulatta		
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecidae; Macaca. 1 (bases 1 to 1119) Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and Tsourushita,N. Cloning of the cDNA encoding L-selectin from nonhuman primates unpublished 2 (bases 1 to 1119) Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and Tsourushita,N. Direct Submission Submitted (08-OCT-1996) Protein Design Labs, Inc., 2375 Garcia Avenue, Mountain View, CA 94043, USA		


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ACCESSION  U26535
VERSION     U26535.1  GI:847787
KEYWORDS
SOURCE
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            Qian,J.
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2001, 01:42:03 ; Search time 52.72 Seconds
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Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

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Maximum DB seq length: 200000000

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2116	100.0	372	14	AAAR37960
2	2116	100.0	372	14	AAAR38908
3	2116	100.0	372	16	AAAR76506
4	2116	100.0	372	16	AAAR83050
5	2116	100.0	372	17	AAAR98106
6	2116	100.0	372	19	AAAR37781
7	2116	100.0	372	20	AAAR73264
8	2110	99.7	371	17	AAAR81122
9	2109	99.7	371	17	AAAR81115
10	2109	99.7	371	17	AAAR98124
11	2109	99.7	372	13	AAAR24026

12	2108	99.6	371	17	AAAR98110	Human lymphocyte c
13	2108	99.6	371	17	AAAR98113	Human lymphocyte c
14	2108	99.6	371	17	AAAR98119	Human lymphocyte c
15	2108	99.6	372	13	AAAR22802	Human lymphocyte h
16	2107	99.6	371	17	AAAR98111	Human lymphocyte c
17	2107	99.6	371	17	AAAR98112	Human lymphocyte c
18	2107	99.6	371	17	AAAR98117	Human lymphocyte c
19	2107	99.6	371	17	AAAR98121	Human lymphocyte c
20	2106	99.5	372	12	AAAR12469	Human lymphocyte ce
21	2105	99.5	371	17	AAAR98116	Human lymphocyte c
22	2105	99.5	371	17	AAAR98118	Human lymphocyte c
23	2105	99.5	371	17	AAAR98120	Human lymphocyte c
24	2105	99.5	371	17	AAAR98123	Human lymphocyte c
25	2104	99.4	371	17	AAAR98109	Human lymphocyte c
26	2103	99.4	371	17	AAAR98114	Human lymphocyte c
27	2100.5	99.3	372	17	AAAR98113	Human lymphocyte c
28	2099.5	99.2	371	17	AAAR98129	Human lymphocyte c
29	2099.5	99.2	374	17	AAAR98131	Human lymphocyte c
30	2099.5	99.2	374	17	AAAR98132	Human lymphocyte c
31	2099.5	99.2	374	17	AAAR98134	Human lymphocyte c
32	2099.5	99.2	374	17	AAAR98135	Human lymphocyte c
33	2096.5	99.1	370	17	AAAR98127	Human lymphocyte c
34	2096.5	99.1	370	17	AAAR98130	Human lymphocyte c
35	2094.5	99.0	370	17	AAAR98126	Human lymphocyte c
36	2094.5	99.0	370	17	AAAR98128	Human lymphocyte c
37	2090	98.8	369	17	AAAR98125	Human lymphocyte c
38	2082	98.4	385	13	AAAR20815	T lymphocyte-speci
39	2082	98.4	385	17	AAAR1442	Human Leu8 antigen
40	2082	98.4	385	19	AAAR60452	Human Leu8 antigen
41	2082	98.4	385	20	AAAR6199	Human Leu8 antigen
42	2082	98.4	385	21	AAAR96138	Human T-cell speci
43	2076	98.1	385	14	AAAR34187	Sequence encoded b
44	2076	98.1	385	15	AAAR56653	L-selectin. Homo
45	2076	98.1	385	18	AAAR21657	Human lymphocyte-a

ALIGNMENTS

RESULT 1	
AAAR37960	standard; Protein: 372 AA.
ID	AAAR37960;
AC	AAAR37960;
XX	
DT	08-OCT-1993 (first entry)
XX	
DE	Human Lymphocyte Homing Receptor.
XX	
KW	HuLHR; lymphocyte binding inhibition: lymphoma metastasis;
KW	transplant rejection; inflammation.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Peptide
FT	Location/Qualifiers
FT	/label= signal_sequence
FT	39..372
FT	/note= "Trp39 is probable N-terminus of mature LHR"
FT	39..155
FT	Domain
FT	/label= Lectin_domain
FT	60..62
FT	/note= "potential N-glycosylation site"
FT	104..106
FT	/note= "potential N-glycosylation site"
FT	160..193
FT	Domain
FT	/label= BGF_domain
FT	177..179
FT	/note= "potential N-glycosylation site"
FT	197..258
FT	/label= Complement_Binding_Repeat_1
FT	216..218
FT	/note= "potential N-glycosylation site"
FT	Modified-site

```

FT Modified-site 232..234
FT /note="potential N-glycosylation site"
FT Modified-site 245..248
FT /note="potential N-glycosylation site"
FT Region 259..317
FT /label="Complement_Binding_Repeat_2"
FT Modified-site 271..273
FT /note="potential N-glycosylation site"
FT Modified-site 311..313
FT /note="potential N-glycosylation site"
FT Domain 333..355
FT /label="Transmembrane_Domain"
FT /note="stop transfer sequence"
FT Domain 356..372
FT /label="Cytoplasmic_Domain"
PN US5216131-A.
XX 01-JUN-1993.
PD
XX
XX 23-FEB-1989; 89US-0315015.
PF
XX
PR 23-FEB-1989; 89US-0315015.
PR 31-OCT-1991; 91US-0786149.
PA (GETH ) GENENTECH INC.
PI Lasky LA, Rosen SD, Slinger MS, Stachel SE, Yednock TA;
PI N-PSDB; AAQ43154.
DR WPI: 1993-188586/23.
DR N-PSDB; AAQ43154.
XX
XX Human and murine lymphocyte homing receptors to treat graft
PT rejection and inflammation - comprise carbohydrate binding,
PT epidermal growth factor and complement binding domains
XX
PS Claim 1; Fig 1 and Fig 3; 32pp; English.
XX
XX A human peripheral blood lymphocyte cDNA library in lambda gt10 was
CC screened with a 2.2kb EcoRI insert of the murine Mel14 antigen clone
CC (1.e. a murine LHR sequence). The largest EcoRI insert (2.2kb) was
CC isolated and sequenced. The ORF codes for 372 amino acids with a mol.
CC wt. of approximately 42,200. Comparison of the HULHR amino acid
CC sequence with the murine LHR sequence (AAR37961) showed a high degree
CC of amino acid conservation in each of the LHR domains, e.g. 96% in
CC the transmembrane domain and 83% in the carbohydrate binding domain.
CC The LHRs could be used to compete with the normal binding of
CC lymphocytes to lymphoid tissue to treat inflammation or graft
CC rejection. They could also be used to control lymphoma metastasis
CC and to treat conditions involving lymphocyte accumulation.
XX
SQ Sequence 372 AA:

```

```

OY 241 CGPFGMNSPEPTCOVYIQCEPLSAPDLGIMNCSHPLASFSFTSACTFTICSEGTLLGKKK 300
DB 241 cgpfgmnspeptcqvlyqceplsapdlgimncshplastsftactfticsegtllgkxx 300
OY 301 TIESSGIMNSPPIQOKLDKSPSMKEGDYNPLFPVAVMTAFSGLAFTIWLARLKK 360
DB 301 tieessgimnsppilcqkldksfsmikegdynplfpvavmvtatfsglaftiwlarrlkk 360
OY 361 GKRSKSRMNDPY 372
DB 361 gkkskrsmndpy 372

```

RESULT 2

```

AAR38908
ID .AAR38908 standard; Protein; 372 AA.
XX
AC AAR38908;
XX
DT 11-JAN-1994 (first entry)
XX
DE HULHR.
XX
KW Human; murine; lymphocyte; cell surface glycoprotein; homing receptor;
KW LHR; endothelium; lymphoid tissue; signal; domain; complement binding;
KW carbohydrate binding; epidermal growth factor-like; egf; intracellular;
KW transmembrane binding; cytoplasmic; ligand binding partner protein;
KW TMD; LBPP.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 20..32
FT /note="Signal peptide"
FT 39..372
FT /note="Mature protein"
FT 39..155
FT /note="Lectin domain"
FT 160..193
FT /note="egf domain"
FT 197..317
FT /note="Complement factor binding domain"
FT 333..355
FT /note="Transmembrane binding domain"
FT 356..372
FT /note="Cytoplasmic domain"
XX
PN US522538-A.
XX
PD 06-JUL-1993.
XX
PE 23-FEB-1989; 89US-0315015.
PR 23-FEB-1989; 89US-0315015.
PR 22-NOV-1989; 89US-0440625.
PR 16-DEC-1991; 91US-0808122.
XX
PA (GETH ) GENENTECH INC.
PI Capon DJ, Lasky LA;
PI WPI: 1993-226664/28.
PI N-PSDB; AAQ44243.
XX
XX New lymphocyte homing receptor immunoglobulin fusion
PT polypeptide(s) - used to inhibit binding of lymphocytes in
PT therapeutic and diagnostic uses
XX
PS Disclosure; Fig 1; 44pp; English.
XX
CC The sequences given in AAR38908-09 represent human and murine lymphocyte
CC cell surface glycoprotein (LHR) respectively. These proteins mediate

```

CC the binding of lymphocytes to the endothelium of lymphoid tissue. LHR
 CC is a glycoprotein which contains a signal domain, a carbohydrate
 CC binding domain, an epidermal growth factor-like (egf) domain, at least
 CC one complement binding domain repeat, a transmembrane binding domain
 CC (TMD) and a charged intracellular or cytoplasmic domain. The murine
 CC and human amino acid sequences show a high degree of overall homology
 CC (83%), however degrees of homology between the various domains is
 CC variable. These proteins may be fused to a ligand binding partner
 CC protein (LBP) which causes an increase in the half life of the LHR.
 CC The fusions may be used therapeutically to compete with the normal
 CC binding of lymphocytes to lymphoid tissue. They may be used in organ
 CC or graft rejection and for the treatment of inflammation.

XX Sequence 372 AA:

Query Match 100.0%; Score 2116; DB 14; Length 372;
 Best Local Similarity 100.0%; Pred. No. 5,4e-141;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPWKCGSTQRDLNMFKMGWTLCCDFLAHGYCWTYHSEKPMNQARARPCRDN 60
 DB 1 mlfpwkcgstqrclnmlfkmgwtmccdfiahgytcwlyhsekpmmwqararrfcrdn 60
 QY 61 YTDLVAIONKAEIEYLEKTLPEFSRYWIGIRKIGIMTWGNTKSLTEBAEMWGDGEPN 120
 DB 61 ytdlvalionkaeieylektlpfsrywigirkgimtwgntkslteeaenwgdgpn 120
 QY 121 NKNKEDCEVIYIKRNKDAGKWNDDACHKALKALCYTASQPCWSCGHGECVEIINNHTC 180
 DB 121 nknkedceviyikrnkdagkwnddachkalkalcytasqpcwscghgeveilinnhtc 180
 QY 181 NCDVGYGPGCOLVIOCEPLEAELGTMCTHPPFGNFSFGSCAFSGSEGTNTGTIEET 240
 DB 181 ncdvgygpgcolviocepleaelgtmcthpfgnfsgscsfasegtntgtieett 240
 QY 241 CGPFGMWSSPEPTCOYIOCEPLSAPDLGIMNCSHPLASFSTACFTICEGTELGGKKR 300
 DB 241 cgpfgmwsspeptcqvioceplsapdlgimncshplastsfscfticegtelelqkkr 300
 QY 301 TICESGIMNSPICOQLDKSFSMKEGDPNLFIPVAVMVTAFSGLAFTIWLARLKK 360
 DB 301 ticesgimnspepicoqldksfsmkegdynlfpvavmvtafsglaftiwlarrlkk 360
 QY 361 GKKSRSKNDPY 372
 DB 361 gkkskrsmndpy 372

RESULT 3

AA76506 standard; Protein: 372 AA.

AA76506;

01-DEC-1995 (first entry)

Human LHR.

Lymphocyte homing receptor; lymphocyte cell surface glycoprotein;

LHR; ligand binding partner; immunoglobulin; constant region;

antibody engineering; immunomodulator.

Homo sapiens.

Location/Qualifiers

Key 20..32 /label= Sig-peptide

Protein 39..372 /note= "hydrophobic domain, may act as signal for insertion into the endoplasmic reticulum lumen"

Label= Mat-protein

FT Domain 39..374 /note= "putative extracellular domain"
 FT Modified-site 60..62 /label= N-glycosylation-site
 FT Modified-site 104..106 /label= N-glycosylation-site
 FT Modified-site 177..179 /label= N-glycosylation-site
 FT Modified-site 216..218 /label= N-glycosylation-site
 FT Modified-site 232..234 /label= N-glycosylation-site
 FT Modified-site 246..248 /label= N-glycosylation-site
 FT Modified-site 271..273 /label= N-glycosylation-site
 FT Modified-site 311..313 /label= N-glycosylation-site
 FT Domain 335..357 /note= "putative stop transfer or membrane anchor domain"
 FT Region 358..372 /note= "putative intracellular region"

PN US5428130-A.
 PD 27-JUN-1995.
 PX 23-FEB-1989; 89US-0315015.
 XX 22-NOV-1989; 89US-0440625.
 PR 23-FEB-1989; 89US-0315015.
 PR 16-DEC-1991; 91US-0808122.
 PR 08-DEC-1992; 92US-0986931.
 XX (GETH) GENENTECH INC.

PI Capon DJ, Lasky LA;

DR WPI: 1995-240086/31.

DR N-PSDB; AAQ92802.

PT New hybrid ligand binding partner molecules - fused to immunoglobulin

PT constant region sequences to increase stability and in vivo plasma

PT half-life

PS Disclosure; Fig. 1a-1c; 40pp; English.

CC A murine Mel 14 antigen cDNA clone was used to screen a lambda gt10

CC cDNA library derived from human peripheral blood lymphocyte mRNA

CC obtd. from primary cells. A cDNA clone encoding LHR was isolated.

XX Sequence 372 AA:

Query Match 100.0%; Score 2116; DB 16; Length 372;
 Best Local Similarity 100.0%; Pred. No. 5,4e-141;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPWKCGSTQRDLNMFKMGWTLCCDFLAHGYCWTYHSEKPMNQARARPCRDN 60
 DB 1 mlfpwkcgstqrclnmlfkmgwtmccdfiahgytcwlyhsekpmmwqararrfcrdn 60
 QY 61 YTDLVAIONKAEIEYLEKTLPEFSRYWIGIRKIGIMTWGNTKSLTEBAEMWGDGEPN 120
 DB 61 ytdlvalionkaeieylektlpfsrywigirkgimtwgntkslteeaenwgdgpn 120
 QY 121 NKNKEDCEVIYIKRNKDAGKWNDDACHKALKALCYTASQPCWSCGHGECVEIINNHTC 180
 DB 121 nknkedceviyikrnkdagkwnddachkalkalcytasqpcwscghgeveilinnhtc 180
 QY 181 NCDVGYGPGCOLVIOCEPLEAELGTMCTHPPFGNFSFGSCAFSGSEGTNTGTIEET 240
 DB 181 ncdvgygpgcolviocepleaelgtmcthpfgnfsgscsfasegtntgtieett 240

Db 181 ncdvgyypgcqlviqceplaeapclgltmndctbpfngfnsfscqafscsegtlntlgieett 240
 QY 241 CGPGNMSSEPTCOVIOCEPLSAPDGIIMNCSHPLASFSTSACTPICSEGTELIGKKR 300
 Db 241 cspignwsspeptcqvlyqceplsapdligimncshplastsfctficscgtelilgkkk 300
 QY 301 TICSSSGIWSNPSPICOKLDKFSFMKEGDNPLFIPIVAVWTAFGSLAFIIMLARLKK 360
 Db 301 ticessglwnspplcqlkldksfsmikegdyndplfipvaavmtafsglatilwlatrllkk 360
 QY 361 GKSKRSKSNMPY 372
 Db 361 gkkskrsmndpy 372

RESULT 4
 AAR83050
 ID AAR83050 standard; Protein; 372 AA.
 AC AAR83050;
 XX
 DT 31-JAN-1996 (first entry)
 XX
 DE Human LHR.

XX Lymphocyte cell surface glycoprotein; LHR; transmembrane receptor;
 KW immunoglobulin; IgG; constant region; receptor-mediated disease;
 KW vector; plasma-life.
 XX
 OS Homo sapiens.

FT key Location/Qualifiers
 FT Peptide 20..32
 FT /label= Sig_peptide
 FT Domain 39..155
 FT /label= Carbohydrate_binding_domain
 FT Domain 160..193
 FT /label= Epidermal_growth_factor_domain
 FT Domain 197..317
 FT /label= Complement_factor_binding_domain
 FT Domain 333..355
 FT /label= Transmembrane_binding_domain
 FT Domain 356..372
 FT /label= Cytoplasmic_domain
 FT /note= "potential stop transfer sequence"
 FT Modified-site 60..62
 FT /label= N-glycosylation_site
 FT Modified-site 104..106
 FT /label= N-glycosylation_site
 FT Modified-site 177..179
 FT /label= N-glycosylation_site
 FT Modified-site 216..218
 FT /label= N-glycosylation_site
 FT Modified-site 232..234
 FT /label= N-glycosylation_site
 FT Modified-site 248..248
 FT /label= N-glycosylation_site
 FT Modified-site 271..273
 FT /label= N-glycosylation_site
 FT Modified-site 311..313
 FT /label= N-glycosylation_site
 XX
 PV US5455165-A.
 XX
 PD 03-OCT-1995.
 XX
 PF 23-FEB-1989; 89US-0315015.
 XX
 PR 22-NOV-1989; 89US-0440625.
 PR 23-FEB-1989; 89US-0315015.
 PR 16-DEC-1991; 91US-0808122.
 PR 08-DEC-1992; 92US-0986931.
 PR 21-JAN-1994; 94US-0185669.

XX (GETH) GENENTECH INC.
 PA Capon DJ, Lasky LA;
 XX
 PI
 XX
 XX MPI: 1995-350776/45.
 DR N-PSDB: AAT05869.
 XX
 PT Expression vector encoding fusion protein to increase plasma life -
 PT comprises receptor ligand binding site and Ig constant region, for
 PT treatment of receptor mediated disease
 XX
 PS Disclosure: Fig 1; 42pp; English.
 XX
 CC A mouse LHR (lymphocyte cell surface glycoprotein) cDNA clone was used
 CC to screen an oligo-dT primed lambda gt10 cDNA library derived from
 CC human peripheral blood lymphocyte mRNA obtd. from primary cells. A
 CC 2.2 kb clone (sequence given in AAT05869) was isolated that encoded the
 CC human LHR protein (AAR83050). LHR-IgG hybrids were constructed for use
 CC in the targeting of therapeutic moieties to lymphoid tissue.
 XX
 SQ Sequence 372 AA;

Query Match 100.0%; Score 2116; DB 16; Length 372;
 Best Local Similarity 100.0%; Pred. No. 5,4e-141;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPWKCOSTORDLWNIKFLMGWTM/CDFLAHHGTVCWYHYSEKPMNQRARPCRDN 60
 Db 1 mifpwkcqstqrdlwnikflmgwtmccdfiahngtvcwtyhysekpmmqrrarrifrdn 60
 QY 61 YTDVAIQNKAEIEYLETTPFSNRYTIGIRKIGITWTVGTVKSLTEAEKMGDEPN 120
 Db 61 ytdvaiaqnkaeyletltprfsryywigirkigigtwtvgtvtnkslteaenwgdepn 120
 QY 121 NKKNKEDCEYIYIRKRNKAGKWNDACHKLKAALCYTASOCPWSCSGHGCVEIINHTC 180
 Db 121 nknkedceveiyirkrnkagkwndachklkaalcycascpwscsgshgcveiinhtc 180
 QY 181 NCDVGYPGCOLVIOCEPLAEAPCLGTMDCTHPPGNFSSOCAFCSCSEGTNLGIEETT 240
 Db 181 ncdvgyypgcqlviqceplaeapclgltmndctbpfngfnsfscqafscsegtlntlgieett 240
 QY 241 CGPGNMSSEPTCOVIOCEPLSAPDGIIMNCSHPLASFSTSACTPICSEGTIELIGKKR 300
 Db 241 cspignwsspeptcqvlyqceplsapdligimncshplastsfctficscgtelilgkkk 300
 QY 301 TICSSSGIWSNPSPICOKLDKFSFMKEGDNPLFIPIVAVWTAFGSLAFIIMLARLKK 360
 Db 301 ticessglwnspplcqlkldksfsmikegdyndplfipvaavmtafsglatilwlatrllkk 360
 QY 361 GKSKRSKSNMPY 372
 Db 361 gkkskrsmndpy 372

RESULT 5
 AAR8106
 ID AAR8106 standard; Protein; 372 AA.
 AC AAR8106;
 XX
 DT 31-OCT-1996 (first entry)
 XX
 DE Human lymphocyte cell surface glycoprotein (HuLHR).

XX Immunoglobulin; transmembrane receptor; adhesion; targeting;
 KW diagnosis; therapy; drug delivery; antiviral; neuromodulator;
 KW immunomodulator; cell adhesion; graft rejection; inflammation;
 KW metastasis.
 XX
 OS Homo sapiens.

```

XX Key Location/Qualifiers
FH Region 1..38
FT /label= Signal region.
FT Domain 39..155
FT /label= Lectin domain.
FT Domain 160..193
FT /label= EGF domain.
FT Binding-site 197..258
FT /label= Complement binding repeat 1.
FT Binding-site 259..317
FT /label= Complement binding repeat 2.
FT Domain 333..355
FT /label= Transmembrane domain.
FT Domain 356..372
FT /label= Cytoplasmic domain.
XX
XX US5514582-A.
XX
XX PD 07-MAY-1996.
XX
XX PE 23-FEB-1989; 89US-0315015.
XX
XX PR 22-NOV-1989; 89US-0440625.
XX PR 23-FEB-1989; 89US-0315015.
XX PR 16-DEC-1991; 91US-0808122.
XX PR 08-DEC-1992; 92US-0986931.
XX PR -21-JAN-1994; 94US-0185670.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Capon DJ, Lasky LA;
XX
XX DR WPI; 1996-238773/24.
XX
XX N-PSDB; AAR98106.
XX
XX PT Nucleic acid encoding hybrid immunoglobulin comprising the ligand
XX binding site of a receptor fused to ig constant region - useful for
XX diagnosis and treatment e.g. of inflammation
XX
XX PS Example 2; Figure 1; 41pp; English.
XX
XX CC A hybrid immunoglobulin chain comprising the ligand binding site of
XX a single transmembrane receptor without an active transmembrane
XX region; fused at its C-terminus with the N-terminus of an
XX immunoglobulin constant region. The receptor is not a member of the
XX immunoglobulin super family, nor a multiple subunit polypeptide
XX encoded by discrete genes. The hybrid immunoglobulin chain combines
XX the adhesion/targeting of a ligand binding partner (LRP) with the
XX effector functions of immunoglobulin and can bind to and/or activate
XX more than one ligand. It can be used diagnostically for the in
XX vitro assay of LBP and their targets; or therapeutically to deliver
XX LBP such as toxins, enzymes, growth factors to particular cells.
XX Typical applications are as antiviral, neuromodulator and
XX immunomodulating agents, or as modulators of cell adhesion (e.g. in
XX treating graft rejection, inflammation, metastasis of lymphoma etc.)
XX The immunoglobulin component increases plasma half life and
XX facilitates purification while deletion of the transmembrane region
XX facilitates recovery, improves aqueous solubility and removes
XX potentially immunogenic epitopes.
XX
XX SQ Sequence 372 AA;

```

Query Match 100.0%; Score 2116; DB 17; Length 372;
 Best local Similarity 100.0%; Pred. No. 5.4e-141;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MIFPMKCGSTQRDILWNIFFKLMGWTMLCCDFLAHHGYCWTYHVSSEKPMNQARRECRDN 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 1 mlfpwkcqesqrdlwnlfkiwgtwmlccdfiahngtycwyhysekpmmnqarrrfdrdn 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 YTDLVAIQNAEIEYLEKTLPEFSRSYWIIGIRKIGIWTWVGTRKSLTEFAENMGDDEPN 120

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```

DB 61 ytdlvaIQNAEIEyleKTLPEfRSyWiGIRkiGIWtWVGtRKSLTEFAENMGDdEPN 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 NKKNKEDCEVEIYIKRNKDAGKWNPDACHKALKALCYTASCPWMSGSGHEVEIINHTC 180
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 121 nknkedceveIyIkRNkdagKwnpdachkAlkaALcytascpwmscsgheveIInhtc 180
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 NCDVGYGPGQOLVIOCEPLAPELGTMDCHPRGNSFSGCAFSCSEGNLTGIEFTT 240
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 181 ncdvgygpgqOLvIOcePLaPElGTMDcHPrgNSfSGcAFSCSEGNLTGIEftT 240
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 241 CGPFGNNSPEPTQVIOCEPLSAPDLGIMNCSHPLASFSTSACTFTCSGETLIGKKK 300
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 241 cgpfgnnspeptqVIOcePLsAPDLgIMncSHpLASFstSActFTCSgetLIgkKk 300
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 TICSSGIWSNPSPICQKLDKFSMIKEGDNPLFIPAVWVTAFSGLAFTIIMLARLKK 360
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 301 tIcSSgIwSnpspIcQkldKfSMIkEGdNpLfIpAvWvTAFsgLaFTIImLaRlKk 360
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 361 GKSKSRSMNDPY 372
   ||||||||||||||
DB 361 gKskSRsmndpy 372
   ||||||||||||||

RESULT 6
AAW37781
ID AAW37781 standard; Protein: 372 AA.
XX
XX AC AAW37781;
XX
XX DT 17-AUG-1998 (first entry)
XX
XX DE Homo sapiens lymphocyte homing receptor (LHR).
XX
XX KW lymphocyte homing receptor; LHR; HuLHR; organ; graft; rejection;
XX treatment; inflammatory disorders; rheumatoid arthritis;
XX autoimmune diseases; lymphoma metastasis; control; lymphocyte;
XX accumulation.
XX
XX OS Homo sapiens.
XX
XX FH Key
XX FT Peptide 20..33
XX FT /note= "potential signal sequence"
XX FT Region 60..62
XX FT /note= "potential N-linked glycosylation site"
XX FT Region 104..106
XX FT /note= "potential N-linked glycosylation site"
XX FT Region 177..179
XX FT /note= "potential N-linked glycosylation site"
XX FT Region 216..218
XX FT /note= "potential N-linked glycosylation site"
XX FT Region 232..234
XX FT /note= "potential N-linked glycosylation site"
XX FT Region 246..248
XX FT /note= "potential N-linked glycosylation site"
XX FT Region 271..273
XX FT /note= "potential N-linked glycosylation site"
XX FT Region 311..313
XX FT /note= "potential N-linked glycosylation site"
XX FT Region 335..357
XX FT /note= "potential N-linked glycosylation site"
XX FT Domain
XX
XX US5714147-A.
XX
XX PN 03-FEB-1998.
XX
XX PD 23-FEB-1989; 89US-0315015.
XX
XX PF 23-NOV-1989; 89US-0440625.
XX PR 23-FEB-1989; 89US-0315015.
XX PR 19-DEC-1991; 91US-0808122.
XX PR 08-DEC-1992; 92US-0986931.

```

PR 21-JAN-1994; 94US-0185670.
 XX 26-MAY-1995; 95US-0451848.
 PA (GETH) GENENTECH INC.
 XX
 PI Capon DJ, Lasky LA;
 XX
 DR WPI: 1998-129805/12.
 DR N-PSDB: AAV19012.
 XX

PT Prevention of lymphocyte attachment to endothelial cells - using
 PT chimeric molecule comprising lymphocyte homing receptor and
 PT immunoglobulin constant region
 PT
 PS
 XX

Disclosure: Fig 1; 43pp: English.

CC The sequence is that of a human lymphocyte homing receptor
 CC (LHR) which may be used in the construction of a chimeric molecule
 CC comprising an LHR fused at its C terminus to the N terminus of an
 CC immunoglobulin constant region. This can be used for the prevention
 CC of lymphocyte attachment to endothelial cells. Such a method may
 CC be used for preventing organ or graft rejection, for treating
 CC inflammatory disorders, e.g. rheumatoid arthritis or other
 CC autoimmune diseases, for controlling lymphoma metastasis and
 CC for treating conditions in which there is an accumulation of
 CC lymphocytes.
 CC
 XX

Sequence 372 AA;

Query Match 100.0%; Score 2116; DB 19; Length 372;
 Best Local Similarity 100.0%; Pred. No. 5.4e-141;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPMKCSQSTQRDLMNIFKLMGWTMLCCDFLAHHGYCWTYHSEKPMNQRRRCRDN 60
 Db 1 mifpmkcsqstqrdlmnifkmgwtmccdflahghgycwtwhysekpnmwqrrrrcrrdn 60
 QY 61 YTDVAIQNKAEIELEYLEKTLPEFSRSYWIIGIRKIGIWTWGTNKSITTEAENMGDEPN 120
 Db 61 ytdvaliqnkaeieleylektlpefsrswywigirkigiwtwgtnkslteaenmgdepn 120
 QY 121 NKKNKEDCVETIYIKRNKDAGKNDACHKILKALCTTASQCPWSCSGHGECVEIINNHTC 180
 Db 121 nknkedcveiyikrnkdagkndachkilaalcyytascpwscsghgveeiinnhct 180
 QY 181 NCDVGYGPGQQLVIOCEPLAEPLGTMDCTHHPGNFSFSSQCAFSCSGTNLTGIEETT 240
 Db 181 ncdvgygpgqqlvioceplaeplgtmdcthhpgnfsfssqcafscsgtnltgieett 240
 QY 241 CGPFGNWSPEPTCOVITQCEPLASAPDLGIMNCSHPLASFSTACTFTICSEGTELIGKKK 300
 Db 241 cgpfgnwspeptcovitqceplaspdlgimncshplasfstsactfticsegteliggkk 300
 QY 301 TICSSGIMWSNPICOKLDKSFMSIKEDGYNPLFIPVAVMTAFSGLAFTIWLARLKK 360
 Db 301 ticssgimwsnpicokldksfmsikedgynplfipvavmtafsglaftiwlarlkk 360
 QY 361 GKKSRSNDPY 372
 Db 361 gkksrsmndpy 372

RESULT 7

AAW73264
 ID AAW73264 standard; Protein: 372 AA.

XX AC AAW73264;

XX DT 02-FEB-1999 (first entry)

XX DE Human lymphocyte homing receptor.

KW Lymphocyte homing receptor; LHR; lymphocyte cell-surface glycoprotein;
 KW lymphocyte binding; endothelium; graft rejection; inflammation; therapy;
 KW arthritis; autoimmune disease; lymphoma metastasis;
 KW lymphocyte accumulation; human.

OS Homo sapiens.

XX US5840844-A.

XX 24-NOV-1998.

PF 10-AUG-1995; 95US-0513278.

PR 23-FEB-1989; 89US-0315015.

PR 31-OCT-1991; 91US-0786149.

PR 06-MAY-1993; 93US-0059029.

PR 10-AUG-1995; 95US-0513278.

PA (GETH) GENENTECH INC.

DR (REGC) UNIT CALIFORNIA.

XX Lasky LA, Rosen SD, Singer MS, Stachel SE;

XX WPI: 1999-034122/03.

XX N-PSDB: AAV08321.

XX Claim 1; Fig 1; 33pp: English.

This sequence is the human lymphocyte homing receptor (LHR) of the
 invention. LHR is a lymphocyte cell-surface glycoprotein that mediates
 the binding of lymphocytes to the endothelium of lymphoid tissue. Soluble
 LHR polypeptides, lacking signal peptide (amino acids 1-38),
 transmembrane domain (amino acids 333-355) and cytoplasmic domain (amino
 acids 356-372), can be used therapeutically to compete with the normal
 binding of lymphocytes to lymphoid tissue and are especially useful for
 organ or graft rejection treatment protocols, for treating inflammations
 such as arthritis and other autoimmune diseases, for control of lymphoma
 metastasis and for treating conditions involving lymphocyte accumulation.
 LHR polypeptides can also be used in assays for LHR, anti-LHR antibodies
 or competitive inhibitors of LHR activity, and for purifying anti-LHR
 antibodies, and as immunogens for raising anti-LHR antibodies.

Sequence 372 AA;

Query Match 100.0%; Score 2116; DB 20; Length 372;
 Best Local Similarity 100.0%; Pred. No. 5.4e-141;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPMKCSQSTQRDLMNIFKLMGWTMLCCDFLAHHGYCWTYHSEKPMNQRRRCRDN 60
 Db 1 mifpmkcsqstqrdlmnifkmgwtmccdflahghgycwtwhysekpnmwqrrrrcrrdn 60
 QY 61 YTDVAIQNKAEIELEYLEKTLPEFSRSYWIIGIRKIGIWTWGTNKSITTEAENMGDEPN 120
 Db 61 ytdvaliqnkaeieleylektlpefsrswywigirkigiwtwgtnkslteaenmgdepn 120
 QY 121 NKKNKEDCVETIYIKRNKDAGKNDACHKILKALCTTASQCPWSCSGHGECVEIINNHTC 180
 Db 121 nknkedcveiyikrnkdagkndachkilaalcyytascpwscsghgveeiinnhct 180
 QY 181 NCDVGYGPGQQLVIOCEPLAEPLGTMDCTHHPGNFSFSSQCAFSCSGTNLTGIEETT 240
 Db 181 ncdvgygpgqqlvioceplaeplgtmdcthhpgnfsfssqcafscsgtnltgieett 240
 QY 241 CGPFGNWSPEPTCOVITQCEPLASAPDLGIMNCSHPLASFSTACTFTICSEGTELIGKKK 300
 Db 241 cgpfgnwspeptcovitqceplaspdlgimncshplasfstsactfticsegteliggkk 300
 QY 301 TICSSGIMWSNPICOKLDKSFMSIKEDGYNPLFIPVAVMTAFSGLAFTIWLARLKK 360

|||||
Db 301 ltessglwsnpspicqlkldksfsmklegdynplflpavmwtafsglatflwarrlkk 360
QY 361 GKSKRSNDPY 372
|||||
Db 361 gkskrsndpy 372

RESULT 8
AAR98122
ID AAR98122 standard; Protein; 371 AA.
XX AAR98122;
XX
XX 01-NOV-1996 (first entry)
XX
XX Human lymphocyte cell surface glycoprotein (HULHR) variant.
XX
XX Immunoglobulin; transmembrane receptor; adhesion; targeting;
KM diagnosis; therapy; drug delivery; antiviral; neuromodulator;
KM immunomodulator; cell adhesion; graft rejection; inflammation;
KM metastasis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Region 1..37
FT /label= Signal region.
FT Domain 38..154
FT /label= Lectin domain.
FT Domain 159..192
FT /label= EGF domain.
FT Binding-site 196..257
FT /label= Complement binding repeat 1.
FT Binding-site 258..316
FT /label= Complement binding repeat 2.
FT Domain 332..354
FT /label= Transmembrane domain.
FT Domain 355..371
FT /label= Cytoplasmic domain.
XX
XX USS514582-A.
XX
XX 07-MAY-1996.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 16-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185670.
XX
XX (GETH) GENENTECH INC.
XX
XX Capon DJ, Laskey LA;
XX
XX WPI; 1996-238773/24.
XX
XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand
PT binding site of a receptor fused to Ig constant region - useful for
PT diagnosis and treatment e.g. of inflammation
XX
XX
XX Disclosure; Page 19; 41pp; English.
XX
XX A hybrid immunoglobulin chain comprising the ligand binding site of
CC a single transmembrane receptor without an active transmembrane
CC region; fused at its C-terminus with the N-terminus of an
CC immunoglobulin constant region. The receptor is not a member of the
CC immunoglobulin super family, nor a multiple subunit polypeptide
CC encoded by discrete genes. The hybrid immunoglobulin chain combines
CC the adhesion/targeting of a ligand binding partner (LBP) with the
CC effector functions of immunoglobulin and can bind to and/or activate

CC more than one ligand. It can be used diagnostically for the in
CC vitro assay of LBP and their targets; or therapeutically to deliver
CC LBP such as toxins, enzymes, growth factors to particular cells.
CC Typical applications are as antiviral, neuromodulating and
CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
CC treating graft rejection; inflammation; metastasis of lymphoma etc.)
CC The immunoglobulin component increases plasma half life and
CC facilitates purification while deletion of the transmembrane region
CC facilitates recovery, improves aqueous solubility and removes
CC potentially immunogenic epitopes. Variants of the human lymphocyte
CC cell surface glycoprotein described in AAR98106 are given in
CC AAR98109-R98135. This variant contains an Ile288Val substitution.
XX
XX SQ Sequence 371 AA:

Query Match 99.7%; Score 2110; DB 17; Length 371;
Best Local Similarity 99.7%; Pred. No. 1.4e-140;
Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPWKCOSTQRDLWNIRKLKGWTLCCDFLAHGTCTWTHYSEKPMNMQRRARFCNDY 61
Db 1 ifpwkcqstqrdlwnlrfklvgwtmccdfllahgltcywthysekpmnwgrrrrfcrdny 60

QY 62 TDLYAIQNKAEIEYLEKTLPEFSRSYWGIRKIGITWGTNLSLFEAEENMGDGEPPN 121
Db 61 tdlvalqnkaeleylcktlpfrsrywiglrklgltwgtwnkslfeaeenwgdgeppn 120

QY 122 KKNKEDCEVEIYIKRNKDGKNDACHKLKLAALCYTASCPWSCSGHGECEVEIINHTCN 181
Db 121 knkedceveiyikrnkdagkndachklkaalcytascqpwssgsgheceveiinhtcn 180

QY 182 CDVGYTGQCQLVIQCEPLAPBLGTWDCTHPRGNSFSSOCASFCEGNLTGIEETTC 241
Db 181 cdvgytgqcqlvqceplapblgtwdcthprgnsfssocafsfcegnltgieettc 240

QY 242 GPGGNMSSPEPTCOVIOCEPLSAPDGLIMNCSHPLASFSTACTFICSGTETLIGRKT 301
Db 241 gpggnmsspeptcqvioceplsapdglimncshplasfstactficsgteteligrkt 300

QY 302 ICESSGIWSNPSPICQKLDKFSFMKRGDYNPLFIPAVWVTAFFSGLAFTIWLARRLKG 361
Db 301 lcessglwsnpspicqlkldksfsmklegdynplflpavmwtafsglatflwarrlkk 360

QY 362 KSKRSNDPY 372
Db 361 kskrsndpy 371

RESULT 9
AAR98115
ID AAR98115 standard; Protein; 371 AA.
XX
XX AAR98115;
XX
XX 01-NOV-1996 (first entry)
XX
XX Human lymphocyte cell surface glycoprotein (HULHR) variant.
XX
XX Immunoglobulin; transmembrane receptor; adhesion; targeting;
KM diagnosis; therapy; drug delivery; antiviral; neuromodulator;
KM immunomodulator; cell adhesion; graft rejection; inflammation;
KM metastasis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Region 1..37
FT /label= Signal region.
FT Domain 38..154
FT /label= Lectin domain.
FT Domain 159..192
FT /label= EGF domain.

```

FT .Binding-site 196..257
FT /label= Complement binding repeat 1.
FT Binding-site 258..316
FT /label= Complement binding repeat 2.
FT Domain 332..354
FT /label= Transmembrane domain.
FT Domain 355..371
FT /label= Cytoplasmic domain.
XX
XX US5514582-A.
XX
XX 07-MAY-1996.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 16-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185670.
XX
XX (GETH ) GENENTECH INC.
XX
XX Capon DJ, Lasky LA;
XX
XX WPI; 1996-238773/24.
XX
XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand
XX binding site of a receptor fused to Ig constant region - useful for
XX diagnosis and treatment e.g. of inflammation
XX
XX Disclosure; Page 19; 41pp; English.
XX
XX A hybrid immunoglobulin chain comprising the ligand binding site of
XX a single transmembrane receptor without an active transmembrane
XX region; fused at its C-terminus with the N-terminus of an
XX immunoglobulin constant region. The receptor is not a member of the
XX immunoglobulin super family, nor a multiple subunit polypeptide
XX encoded by discrete genes. The hybrid immunoglobulin chain combines
XX the adhesion/targeting of a ligand binding partner (LBP) with the
XX effector functions of immunoglobulin and can bind to and/or activate
XX more than one ligand. It can be used diagnostically for the in
XX vitro assay of LBP and their targets; or therapeutically to deliver
XX LBP such as toxins, enzymes, growth factors to particular cells.
XX Typical applications are as antiviral, neuromodulating and
XX immunomodulating agents, or as modulators of cell adhesion (e.g. in
XX treating graft rejection; inflammation; metastasis of lymphoma etc.)
XX The immunoglobulin component increases plasma half life and
XX facilitates purification while deletion of the transmembrane region
XX facilitates recovery. Improves aqueous solubility and removes
XX potentially immunogenic epitopes. Variants of the human lymphocyte
XX cell surface glycoprotein described in AAR98106 are given in
XX AAR98109-R98135. This variant contains an Ile174Leu substitution.
XX
XX Sequence 371 AA:
SQ

```

```

Query Match 99.7%; Score 2109; Db 17; Length 371;
Best Local Similarity 99.7%; Pred. No.1,7e-140;
Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 2 IFPMKCGSTGRDLNMFRIKMGWMLCCDFLAHGGTYCWYHSEKPMWQRAARECRDNY 61
DB 1 ifpwkcgstgrdlmifkmgwmlccdflahggtycwyhsekpwmwqrarercrdny 60
QY 62 TDVATLONKAELEYEKLTPESRSYYWTGIRGIMTWGWNKSLTBEAEWGGGEPRNN 121
DB 61 tdvatlonkaeleyekltpeksyywtgirkgtmwtgwnksltbeaewgggeprnn 120
QY 122 KKNKEDCEVEIYIKRNKDGKWNDDACHKIKALCYTASQPSGSGHGEVIEIINNHTCN 181
DB 121 knkedceveiyikrnkdgkwnddachkikaalcytasqpsgsghgeveielinnhtcn 180

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QY 182 CDVGYGPOCOLYIOCEPLEAPELGTMDCTHPRGNFSFSSCAFSCSEGNLTGIEETTC 241
DB 181 cdvgygppgcqlviqcepleapelgtdmcthpignfsfsgcafsesqelnltgiettc 240
QY 242 GPRGNMSSPEPTCQVIQCEPLSAPDGLMNCSHPLASFSFTSACYFICSEGTGKRRY 301
DB 241 gprgnwsspeptcqvliqceplsapdglmncshplastsfctficegtelgkrrt 300
QY 302 ICSSSGIWSNPSPIQCKLCKSPSMKEGDPNPLFIVAAVMVAFSGLATIIMLARLRKG 361
DB 301 icessgiwsnpspicqlcklckspsmkegdpnplfivavmvafsglatiimlarlrkg 360
QY 362 KKSRSMDNDPY 372
DB 361 kksrsmndpy 371

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RESULT 10
AAR98124
ID AAR98124 standard; Protein; 371 AA.
XX
XX AAR98124;
XX
XX 01-NOV-1996 (first entry)
XX
XX Human Lymphocyte cell surface glycoprotein (HULHR) variant.
XX
XX Immunoglobulin; transmembrane receptor; adhesion; targeting;
XX diagnosis; therapy; drug delivery; antiviral; neuromodulator;
XX immunomodulator; cell adhesion; graft rejection; inflammation;
XX metastasis.
XX
XX Homo sapiens.
XX
XX OS
XX
XX Key Location/Qualifiers
XX Region 1..37
XX Domain 38..154
XX Domain 159..192
XX Domain 196..257
XX Binding-site /label= EGF domain.
XX Binding-site /label= Complement binding repeat 1.
XX Binding-site 258..316
XX Binding-site /label= Complement binding repeat 2.
XX Domain 332..354
XX Domain /label= Transmembrane domain.
XX Domain 355..371
XX Domain /label= Cytoplasmic domain.
XX
XX US5514582-A.
XX
XX 07-MAY-1996.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 16-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185670.
XX
XX (GETH ) GENENTECH INC.
XX
XX Capon DJ, Lasky LA;
XX
XX WPI; 1996-238773/24.
XX
XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand
XX binding site of a receptor fused to Ig constant region - useful for
XX diagnosis and treatment e.g. of inflammation
XX
XX Disclosure; Page 19; 41pp; English.

```

XX A hybrid immunoglobulin chain comprising the ligand binding site of
 CC a single transmembrane receptor without an active transmembrane
 CC region; fused at its C-terminus with the N-terminus of an
 CC immunoglobulin constant region. The receptor is not a member of the
 CC immunoglobulin super family, nor a multiple subunit polypeptide
 CC encoded by discrete genes. The hybrid immunoglobulin chain combines
 CC the adhesion/targeting of a ligand binding partner (LBP) with the
 CC effector functions of immunoglobulin and can bind to and/or activate
 CC more than one ligand. It can be used diagnostically for the in
 CC vitro assay of LBP and their targets; or therapeutically to deliver
 CC LBP such as toxins, enzymes, growth factors to particular cells.
 CC Typical applications are as antiviral, neuromodulating and
 CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
 CC treating graft rejection, inflammation; metastasis of lymphoma etc.)
 CC The immunoglobulin component increases plasma half life and
 CC facilitates purification while deletion of the transmembrane region
 CC facilitates recovery, improves aqueous solubility and removes
 CC potentially immunogenic epitopes. Variants of the human lymphocyte
 CC cell surface glycoprotein described in AAR98106 are given in
 CC AAR98109-R98135. This variant contains an Ile302Leu substitution.
 CC
 SQ Sequence 371 AA:

Query Match 99.7%; Score 2109; DB 17; Length 371;
 Best Local Similarity 99.7%; Pred. No. 1.7e-140;

Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 IFPPKQSTQRLDMLNIFKMGWTLCCDFLAHHGTICWTYHSEKPMNQRRRCRDNY 61
 DB 1 ifppkqstqrdlwnlfkmgwtlccdflahhgticwtcyhsekpmnqrrrrcndy 60
 OY 62 TDLVAIQNKAETLEYLEKTLPFSSRYWIGIRKIGITWVGINKSLTEAEKNGDEPN 121
 DB 61 tdlvaliqnkaeyleytlektpfssrywyigirkiiglitwvginkslteaeengdepn 120
 OY 122 KKKKECCVEIYIKRNKDACWMDACHKIKALCYTASQPMSCSGHGCEVEIINNHTCN 181
 DB 121 kkkkedcveiyikrnkdagkwmdachkikaalcytascqpmwscsghgceveilnnhtcn 180
 OY 182 CDVGYGPOCOLVIOCEPELEAPELGTMDCTHPRGNFSFSSQAFSCSEGNLTGIEETTC 241
 DB 181 cdvgygppocqlviqcepeleapeligtmctchprgnfssqafscsegnltgieettc 240
 OY 242 GPFGNMSSPEPTCQVITQCEPLSAPDLGINNCSPHLASFSTSACTPCTCSEGTLLGKKKT 301
 DB 241 gpfgnmsspeptcqvitiqceplsapdlgimncshplasfstsactpctcsegtellgkkkt 300
 OY 302 ICSSSGIWSNPSPICQKLDKSFNKEGQYNPFIYVAVWVTFSGLAFTIWLARLAKG 361
 DB 301 icsssgiwsnpspicqkldksfsmikegdynpfiyvaavwvtafsglaftiwlarrlkg 360
 OY 362 KKSRSRMNDPY 372
 DB 361 kkskrsmndpy 371

RESULT 11
 AAR24026
 ID AAR24026 standard; Protein: 372 AA.
 XX
 AC AAR24026;
 XX
 DT 22-NOV-1992 (first entry)
 XX
 DE Sequence of human lymphocyte cell surface glycoprotein
 DE (HLAHR).
 XX
 KW Lymphocyte cell surface glycoprotein; ligand binding protein.
 XX
 OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Peptide 20..38
 FT /label= signal
 FT Modified-site 60..62
 FT /label= potential N-linked glycosylation site
 FT Modified-site 104..106
 FT /label= see above
 FT Modified-site 177..179
 FT /label= see above
 FT Modified-site 216..218
 FT /label= see above
 FT Modified-site 232..234
 FT /label= see above
 FT Modified-site 271..273
 FT /label= see above
 FT Modified-site 311..313
 FT /label= see above
 FT Region 333..355
 FT /label= stop transfer sequence

XX US5116964-A.
 XX
 PD 26-MAY-1992.
 XX
 PF 22-NOV-1989; 89US-0440625.
 XX
 PR 23-FEB-1989; 89US-0315015.
 PR 22-NOV-1989; 89US-0440625.
 XX

PA (GETH) GENENTECH INC.

PI Capon DJ, Lasky LA;

XX WPI: 1992-199589/24.

DR N-PSDB; AAQ24987.

XX

PT Nucleic acid encoding polypeptide fusions - comprising ligand
 binding partner protein and immunoglobulin chain, for use in

PT

PS

XX

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

SQ Sequence 372 AA:

Query Match 99.7%; Score 2109; DB 13; Length 372;
 Best Local Similarity 99.7%; Pred. No. 1.7e-140;

Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MIFPPKQSTQRLDMLNIFKMGWTLCCDFLAHHGTICWTYHSEKPMNQRRRCRDNY 60
 DB 1 mifppkqstqrdlwnlfkmgwtlccdflahhgticwtcyhsekpmnqrrrrcndy 60
 OY 61 YTPDLVAIQNKAETLEYLEKTLPFSSRYWIGIRKIGITWVGINKSLTEAEKNGDEPN 120
 DB 61 ytpdlvaliqnkaeyleytlektpfssrywyigirkiiglitwvginkslteaeengdepn 120
 OY 121 NKKKKECCVEIYIKRNKDACWMDACHKIKALCYTASQPMSCSGHGCEVEIINNHTCN 180
 DB 121 nkkkedcveiyikrnkdagkwmdachkikaalcytascqpmwscsghgceveilnnhtcn 180

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OY 181 NCDVGYGPOCLVIQCEPLAEPLGTMDCTHPFGNFSFSSQCARSCSEGTNLNGIEETT 240
DB 181 ncdvgygppcqlviqcepleapeplgtmdcthpfgnfsfssqcarsscsegtnlngieelt 240
OY 241 CGPFGWMSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTSACTFTCSGTTELIGRKK 300
DB 241 cgpfgwmspeptcqvioceplsapdlgimncshplasfstsaactftcsegteeligk 300
OY 301 TICSSGIMWNSPPTCOKLDKSFMSIKGSDYNPLFIPAVAVWTAFSGLAFITIMLARLKK 360
DB 301 ticesgimwnspptcqlkdxsfmsikgdy nplfipavavwtatfsglatifliwlarlkk 360
OY 361 GKSKRSNMNDPY 372
DB 361 gksksrsmndpy 372

RESULT 12
AAR98110
ID AAR98110 standard; Protein; 371 AA.
XX
AC AAR98110;
XX
DT 01-NOV-1996 (first entry)
XX
XX Human lymphocyte cell surface glycoprotein (HULHR) variant.
DE
XX Immunoglobulin: transmembrane receptor; adhesion; targeting;
KW diagnosis; therapy; drug delivery; antiviral; neuromodulator;
KW immunomodulator; cell adhesion; graft rejection; inflammation;
XX metastasis.
XX Homo sapiens.
XX OS
XX
XX Key Location/Qualifiers
FH Region 1..37
FT /label= Signal region.
FT Domain 38..154
FT /label= Lectin domain.
FT Domain 159..192
FT /label= EGF domain.
FT Binding-site 196..257
FT /label= Complement binding repeat 1.
FT Binding-site 258..316
FT /label= Complement binding repeat 2.
FT Domain 332..354
FT /label= Transmembrane domain.
FT Domain 355..371
FT /label= Cytoplasmic domain.
XX
XX US5514582-A.
XX
XX 07-MAY-1996.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 16-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185670.
XX
XX (GETH ) GENENTECH INC.
XX
XX Capon DJ, Lasky LA;
XX
XX WPI, 1996-238773/24.
XX
XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand
XX binding site of a receptor fused to Ig constant region - useful for
XX diagnosis and treatment e.g. of inflammation

```

```

PS Disclosure; Page 19; 41pp; English.
XX
XX A hybrid immunoglobulin chain comprising the ligand binding site of
CC a single transmembrane receptor without an active transmembrane
CC region; fused at its C-terminus with the N-terminus of an
CC immunoglobulin constant region. The receptor is not a member of the
CC immunoglobulin super family, nor a multiple subunit polypeptide
CC encoded by discrete genes. The hybrid immunoglobulin chain combines
CC the adhesion/targeting of a ligand binding partner (LBP) with the
CC effector functions of immunoglobulin and can bind to and/or activate
CC more than one ligand. It can be used diagnostically for the in
CC vitro assay of LBP and their targets; or therapeutically to deliver
CC LBP such as toxins, enzymes, growth factors to particular cells.
CC Typical applications are as antiviral, neuromodulating and
CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
CC treating graft rejection; inflammation; metastasis of lymphoma etc.)
CC The immunoglobulin component increases plasma half life and
CC facilitates purification while deletion of the transmembrane region
CC facilitates recovery, improves aqueous solubility and removes
CC potentially immunogenic epitopes. Variants of the human lymphocyte
CC cell surface glycoprotein described in AAR98106 are given in
CC AAR98109-R98135. This variant contains an Ala71Ser substitution.
XX
XX SQ Sequence 371 AA:
XX
XX Query Match 99.6%; Score 2108; DB 17; Length 371;
XX Best Local Similarity 99.7%; Pred. No. 2e-140;
XX Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 2 IPPWKGOSQORDLIMNIFKMGWTMLCCDFIAHHGYCTHYHSEKPMWQARRRRCNDY 61
DB 1 ifpwkcgstgrdlwnlflkfwgwtmccdfiahnglycwtlyhsekpmwqarrircndy 60
OY 62 TDVAIQNKAEILEYLEKTLPSRSYTWIGIRKIGITWGTNKSLTLEAENMGDGEPPNN 121
DB 61 tdlvaliqnkaleylektlpsrswytwigirkgitwgtntkslteaenmgdgsppnn 120
OY 122 KKNKEDCWEIYIKRNKDKGKNDACHTLKAALCYTASQCPWSCSGHGEVEIINHTCN 181
DB 121 knknedcweilykrnkdkgkndachtklaalcytascqpwscsgghgeveilnhntcn 180
OY 182 CDVGYGPOCLVIQCEPLAEPLGTMDCTHPFGNFSFSSQCARSCSEGTNLNGIEETT 241
DB 181 cdvgygppcqlviqcepleapeplgtmdcthpfgnfsfssqcarsscsegtnlngieelt 240
OY 242 GPFGWMSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTSACTFTCSGTTELIGRKK 301
DB 241 gpfgnwmspeptcqvioceplsapdlgimncshplasfstsaactftcsegteeligk 300
OY 302 ICSSGIMWNSPPTCOKLDKSFMSIKGSDYNPLFIPAVAVWTAFSGLAFITIMLARLKK 361
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OY 362 KKSRSNMNDPY 372
DB 361 kksksrsmndpy 371

RESULT 13
AAR98113
ID AAR98113 standard; Protein; 371 AA.
XX
AC AAR98113;
XX
XX 01-NOV-1996 (first entry)
XX
XX Human lymphocyte cell surface glycoprotein (HULHR) variant.
DE
XX Immunoglobulin: transmembrane receptor; adhesion; targeting;
KW diagnosis; therapy; drug delivery; antiviral; neuromodulator;
KW immunomodulator; cell adhesion; graft rejection; inflammation;
KW metastasis.

```

XX	OS	Homo sapiens.
XX	PH	Key
XX	FT	Region
XX	FT	Domain
XX	FT	Domain
XX	FT	Blinding-site
XX	FT	Blinding-site
XX	FT	Blinding-site
XX	FT	Domain
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XX	FT	Domain
XX	PN	US5514582-A.
XX	PD	07-MAY-1996.
XX	XX	23-FEB-1989;
XX	PF	89US-0315015.
XX	XX	22-NOV-1989;
XX	PR	89US-0440625.
XX	PR	23-FEB-1989;
XX	PR	89US-0315015.
XX	PR	16-DEC-1991;
XX	PR	91US-0808122.
XX	PR	08-DEC-1992;
XX	PR	92US-0986931.
XX	PR	21-JAN-1994;
XX	XX	94US-0185670.
XX	PA	(GETH) GENENTECH INC.
XX	PI	Capon DJ, Lasky LA;
XX	XX	WPI: 1996-238773/24.
XX	PT	Nucleic acid encoding hybrid immunoglobulin comprising the ligand
XX	PT	binding site of a receptor fused to Ig constant region - useful for
XX	PT	diagnosis and treatment e.g. of inflammation
XX	PS	Disclosure: Page 19; 41pp; English.
XX	CC	A hybrid immunoglobulin chain comprising the ligand binding site of
XX	CC	a single transmembrane receptor without an active transmembrane
XX	CC	region; fused at its C-terminus with the N-terminus of an
XX	CC	immunoglobulin constant region. The receptor is not a member of the
XX	CC	immunoglobulin super family, nor a multiple subunit polypeptide
XX	CC	encoded by discrete genes. The hybrid immunoglobulin chain combines
XX	CC	the adhesion/targeting of a ligand binding partner (LBP) with the
XX	CC	effector functions of immunoglobulin and can bind to and/or activate
XX	CC	more than one ligand. It can be used diagnostically for the in
XX	CC	vitro assay of LBP and their targets, or therapeutically to deliver
XX	CC	LBP such as toxins, enzymes, growth factors to particular cells.
XX	CC	Typical applications are as antiviral, neuromodulating and
XX	CC	immunomodulating agents, or as modulators of cell adhesion (e.g. in
XX	CC	treating graft rejection; inflammation; metastasis of lymphoma etc.)
XX	CC	The immunoglobulin component increases plasma half life and
XX	CC	facilitates purification while deletion of the transmembrane region
XX	CC	facilitates recovery, improves aqueous solubility and removes
XX	CC	potentially immunogenic epitopes. Variants of the human lymphocyte
XX	CC	cell surface glycoprotein described in AAR8106 are given in
XX	CC	AAR8109-R8135. This variant contains a Leu150Val substitution.
XX	SO	Sequence 371 AA;
XX	XX	Query Match 99.6%; Score 2108; DB 17; Length 371;
XX	XX	Best Local Similarity 99.7%; Pred. No. 2e-140;
XX	XX	Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db	61	tdlvaIQKkaeylekTLPEPSrsyWwIGIRkIGIwTWGTnKSLTNEaENMGDEpN	120
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Qy	182	CDVGYGHCOCULVIOCEPLEAPELGTMDCTHPFCNFSPSSQCAFSCEGNTLGIETTC	241
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AC	AAR98119;		
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DT	01-NOV-1996 (first entry)		
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DE	Human lymphocyte cell surface glycoprotein (HULHR) variant.		
XX			
KM	Immunoglobulin; transmembrane receptor; adhesion; targeting;		
KW	diagnosis; therapy; drug delivery; antiviral; neuromodulator;		
KW	immunomodulator; cell adhesion; graft rejection; inflammation;		
KW	metastasis.		
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FH	Key		
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FT	355..371		
FT	Domain		
FT	/label= Cytoplasmic domain.		
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PD	07-MAY-1996.		
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FE	23-FEB-1989;		
XX	89US-0315015.		
PR	22-NOV-1989;		
XX	89US-0440625.		
PR	23-FEB-1989;		
XX	89US-0315015.		
PR	16-DEC-1991;		
XX	91US-0808122.		
PR	08-DEC-1992;		
XX	92US-0986931.		
PR	21-JAN-1994;		
XX	94US-0185670.		
PA	(GETH) GENENTECH INC.		

XX Capon DJ, Lasky LA;
 PI
 XX
 DR WPI: 1996-238773/24.

PT Nucleic acid encoding hybrid immunoglobulin comprising the ligand
 binding site of a receptor fused to Ig constant region - useful for
 PT diagnosis and treatment e.g. of inflammation

PS Disclosure: Page 19; 41pp; English.

XX A hybrid immunoglobulin chain comprising the ligand binding site of
 CC a single transmembrane receptor without an active transmembrane
 CC region; fused at its C-terminus with the N-terminus of an
 CC immunoglobulin constant region. The receptor is not a member of the
 CC immunoglobulin super family, nor a multiple subunit polypeptide
 CC encoded by discrete genes. The hybrid immunoglobulin chain combines
 CC the adhesion/targeting of a ligand binding partner (LBP) with the
 CC effector functions of immunoglobulin and can bind to and/or activate
 CC more than one ligand. It can be used diagnostically for the in
 CC vitro assay of LBP and their targets; or therapeutically to deliver
 CC LBP such as toxins, enzymes, growth factors to particular cells.
 CC Typical applications are as antiviral, neuromodulating and
 CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
 CC treating graft rejection, inflammation; metastasis of lymphoma etc.)
 CC The immunoglobulin component increases plasma half life and
 CC facilitates purification while deletion of the transmembrane region
 CC facilitates recovery, improves aqueous solubility and removes
 CC potentially immunogenic epitopes. Variants of the human lymphocyte
 CC cell surface glycoprotein described in AAR98106 are given in
 CC AAR98109-R98135. This variant contains a Ser226Thr substitution.

XX Sequence 371 AA;

Query Match 99.6%; Score 2108; DB 17; Length 371;
 Best Local Similarity 99.7%; Pred. No. 2e-140;

Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 TDLVAIQNKAETIYKLPFSRSYWIIGRIKIGITWVGTKSLTEBAENWGDEPN 120
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 DB 241 GPPGNMSSPEPPICQVIOCEPEAPELATMDCTHPGFNFSSQAFSCSEGTNLGIEETTC 300
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 DB 301 ICESGIGWNPSPICOKLDKFSMKEGDYNPFIYVAVWAFSGIAFIILARIRKKG 360
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 DB 361 KSKRSMDPY 371

RESULT 15
 AAR22802
 ID AAR22802 standard; Protein; 372 AA.
 XX
 AC AAR22802;

XX 01-SEP-1992 (first entry)
 DE Human lymphocyte homing receptor.
 XX
 KW HuLHR: LHR: binding; endothelium; immunogens; graft; organ;
 KW rejection; inflammation; rheumatoid arthritis; lymphoma metastasis.
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 OS Homo sapiens.
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 FT /note="N-glycosylation site"
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 FT /note="N-glycosylation site"
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 FT Modified-site 232..234
 FT /note="N-glycosylation site"
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 FT Modified-site 311..313
 FT /note="N-glycosylation site"
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 FT /note="stop transfer or membrane anchoring domain"
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 PN US5098833-A.
 PD 24-MAR-1992.
 XX
 PF 23-FEB-1989; 89US-0315015.
 XX
 PR 23-FEB-1989; 89US-0315015.
 XX
 PA (REGC) UNIV OF CALIFORNIA.
 PI Lasky LA, Rosen SD, Stachel SE, Slinger MS, Yednock TA;
 PI WPI: 1992-123385/15.
 DR N-PSDB; AAQ23623.
 PT New DNA encoding at least one domain of lymphocyte homing
 PT receptor - useful for treating graft rejection, inflammation,
 PT etc.
 PS Disclosure: Fig 1; 32pp; English.
 XX
 CC The protein sequence was deduced from the DNA sequence obt'd. by
 CC screening an oligo dT primed lambda gt10 cDNA library derived from
 CC human peripheral blood lymphocyte mRNA obt'd. from primary cells,
 CC with a 2.2 kb EcoRI insert of the murine Mel 14 antigen cDNA clone.
 CC The protein contains regions encoding a carbohydrate binding domain,
 CC an EGF-like domain, a complement binding domain and a transmembrane
 CC domain. The protein contains 26 cysteine residues. Cells transformed
 CC by the LHR DNA are used to produce LHR (which mediates binding of
 CC lymphocytes to the endothelium of lymphoid tissue). LHR or its
 CC variants are useful as reagents for assaying LHR or anti-LHR anti-
 CC bodies, to purify the antibodies, as immunogens, and therapeutically
 CC to compete with normal binding of lymphocytes (to prevent graft/organ
 CC rejection; to treat inflammation (such as rheumatoid arthritis or
 CC other autoimmune diseases); for control of lymphocyte metastasis,
 CC and to treat conditions associated with accumulation of lymphocytes).
 CC Derivs. and variants of LHR may be produced having modified
 CC properties, e.g. increased activity, longer plasma half-life,
 CC reduced side effects and better aq. solubility.
 CC See also AAR22803.
 XX
 SQ Sequence 372 AA;

Query Match 99.6%; Score 2108; DB 13; Length 372;
Best Local Similarity 99.5%; Pred. No. 2e-140; 1; Indels 0; Gaps 0;
Matches 370; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIPPMKQSTORDLWNIETKLMGWTMLCCDFLAHGTVCWTYHYSEKPMNQARARPCRDN 60
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QY 61 YTDLVAIQNKAEIEYLEKTLPFSSRYTWIGIRKIGIWTWGTNKSLTBEAENMGDEPN 120
|||||
Db 61 ytdlvaiqnkaeylektilpfssrytwigirkgiwtwgtlnkslteeaenwgdepn 120
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QY 121 NKKNKEDCVETIYIKRNMDAGKNDACHKILKALCYTASQCPWSCSGHGECEIINNHTC 180
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QY 181 NCDVGYGPOCQLVIOCEPLEAPELGTMDCTHPFGNPFSSQCAFSCSEGTNLGIEET 240
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QY 361 GKKSRSMDPY 372
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Db 361 gkksrsmndpy 372
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Search completed: October 13, 2001, 02:53:58
Job time: 4315 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 13, 2001, 02:43:42 ; Search time 25.01 Seconds
(without alignments)
306.262 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116
Sequence: 1 MIFPMKCQSTQRDLNIFKL.....WLANRLKKGKKSRKSNNDPY 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents, AA:*

- 1: /cgnl_7/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgnl_7/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgnl_7/ptodata/1/1aa/6A_COMB.pep:*
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- 5: /cgnl_7/ptodata/1/1aa/PCRTUS_COMB.pep:*
- 6: /cgnl_7/ptodata/1/1aa/Backfiles1.pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2116	100.0	372	2	US-08-513-278-2
2	2116	100.0	372	6	US-08-513-278-2
3	2076	98.1	385	1	US-08-340-539A-2
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5	1651	78.0	372	2	US-08-513-278-4
6	1651	78.0	372	6	US-08-513-278-4
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8	899	42.5	830	5	PCR-US91-05059-2
9	889	42.0	830	6	5378464-2
10	862	40.7	610	1	US-08-365-470-3
11	862	40.7	610	1	US-09-209-668-19
12	862	40.7	610	6	5217870-2
13	814.5	38.5	484	2	US-08-252-493C-9
14	814.5	38.5	484	3	US-09-276-197-9
15	666	31.5	117	1	US-08-274-661B-38
16	587	27.7	119	1	US-08-340-539A-14
17	572	27.0	119	1	US-08-340-539A-12
18	569	26.9	119	1	US-08-340-539A-13
19	565	26.7	117	6	5514582-7
20	487	23.0	126	6	5514582-31
21	467	22.1	119	1	US-08-340-539A-18
22	457	22.6	119	1	US-08-340-539A-17
23	452	21.4	119	1	US-08-340-539A-16
24	451	21.3	119	1	US-08-340-539A-19
25	450	21.3	120	1	US-08-274-661B-37
26	445	21.0	117	1	US-08-274-661B-39
27	431	20.4	120	1	US-08-274-661B-36

28	427	20.2	119	1	US-08-340-539A-15	Sequence 15, Appl
29	337	15.9	574	6	5378464-3	Patent No. 5378464
30	237	11.2	67	3	US-08-840-062-8	Sequence 8, Appl
31	199	9.4	36	1	US-08-340-539A-22	Sequence 22, Appl
32	189.5	9.0	1019	1	US-08-296-014A-4	Sequence 4, Appl
33	189.5	9.0	1019	2	US-08-596-405-4	Sequence 4, Appl
34	189.5	9.0	1019	2	US-08-877-620-4	Sequence 4, Appl
35	189.5	9.0	1083	2	US-08-296-014A-2	Sequence 2, Appl
36	189.5	9.0	1083	2	US-08-596-405-2	Sequence 2, Appl
37	189.5	9.0	1083	3	US-08-877-620-2	Sequence 3, Appl
38	181.5	8.6	240	3	US-08-824-692-23	Sequence 23, Appl
39	177	8.4	36	1	US-08-340-539A-20	Sequence 20, Appl
40	175.5	8.3	216	3	US-08-824-692-24	Sequence 24, Appl
41	172	8.1	1466	6	5256642-6	Patent No. 5256642
42	172	8.1	1466	6	5472939-6	Patent No. 5472939
43	172	8.1	1537	6	5256642-5	Patent No. 5256642
44	172	8.1	1537	6	5472939-5	Patent No. 5472939
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ALIGNMENTS

RESULT 1
US-08-513-278-2
Sequence 2, Application US/08513278
Patent No. 5840844
GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: YEDNOK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,278
FILING DATE: 10-AUG-1995
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059027
FILING DATE: 06-MAY-1993
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/315015
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Dregler, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 565D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-513-278-2

Query Match 100.0%; Score 2116; DB 2; Length 372;
 Best Local Similarity 100.0%; Pred. No. 2,9e-185;
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 QY 121 NKKNEDEVETIYIKRNKAGKNDACHKLAALCYTASCPMCSGHECEVEIINNHTC 180
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RESULT 2
 5514582-2
 ; Patent No. 5514582
 ; APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.
 ; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
 ; IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 43
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/185,670
 ; FILING DATE: 21-JAN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 986,931
 ; FILING DATE: 08-DEC-1992
 ; APPLICATION NUMBER: 808,122
 ; FILING DATE: 16-DEC-1991
 ; APPLICATION NUMBER: 440,625
 ; FILING DATE: 22-NOV-1989
 ; APPLICATION NUMBER: 315,015
 ; FILING DATE: 23-FEB-1989
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 DB 181 NCDVGYGPOCQVIOCEPLAPDLGIMNCSPHPLASFSTACTICSEGTNLGIEETT 240
 QY 241 CGPFGNMSPEPTCOVIOCEPLAPDLGIMNCSPHPLASFSTACTICSEGTNLGIEETT 300
 DB 241 CGPFGNMSPEPTCOVIOCEPLAPDLGIMNCSPHPLASFSTACTICSEGTNLGIEETT 300
 QY 301 TICSSGSIWNSPPIQCKLDRSFMKEGDYNPLFIPVAVMTAFSGLAFTIWLARLKK 360
 DB 301 TICSSGSIWNSPPIQCKLDRSFMKEGDYNPLFIPVAVMTAFSGLAFTIWLARLKK 360
 QY 361 GKRSKRSMDPY 372
 DB 361 GKRSKRSMDPY 372

RESULT 3
 US-08-340-539A-2
 ; Sequence 2, Application US/08340539A
 ; Patent No. 5808025
 ; GENERAL INFORMATION:
 ; APPLICANT: Tedder, Thomas F.
 ; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
 ; BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FISH & NEAVE
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10020
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/340,539A
 ; FILING DATE: 16-NOV-1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/008,459
 ; FILING DATE: 25-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gunnison, Jane
 ; REGISTRATION NUMBER: 38,479
 ; REFERENCE/DOCKET NUMBER: CG-104 CON
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-596-9000
 ; TELEFAX: 212-596-9090
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 385 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-340-539A-2

Query Match 98.1%; Score 2076; DB 1; Length 385;
 Best Local Similarity 98.1%; Pred. No. 1,3e-181;
 Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIEPWCOSTORDLNNIRKMGWMLCCDFLAHGTCTHYHSEKPMNWRARFCHDN 60
 DB 14 MIEPWCOSTORDLNNIRKMGWMLCCDFLAHGTCTHYHSEKPMNWRARFCHDN 73
 QY 61 YTDVAIONKAEIELEKTLPEFSRSYTWIGIRKIGITWTWGTNKSLEEAENMGDGEPN 120

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Db      74 YTDLVAIONKAEIEYLEKTLPEFSRSYIWKIRKIGITWTWGTNKSLTLEAENKGDSEPN 133
      121 NKKNEDECEVEIYIKRNKDAGKNDACCHKLKAALCYTASCPWSCSGHGEVEIINNHTC 180
      134 NKKNEDECEVEIYIKRNKDAGKNDACCHKLKAALCYTASCPWSCSGHGEVEIINNHTC 193
      181 NCDVGYGPOCQVYIOCEPLAPDLGIMNCSHPLASFSTACTPICSSEGTLLGIEETT 240
      194 NCDVGYGPOCQVYIOCEPLAPDLGIMNCSHPLASFSTACTPICSSEGTLLGIEETT 253
      241 CGPFGNWSPEPTCQVYIOCEPLAPDLGIMNCSHPLASFSTACTPICSSEGTLLGIEETT 300
      254 CGPFGNWSPEPTCQVYIOCEPLAPDLGIMNCSHPLASFSTACTPICSSEGTLLGIEETT 313
      301 TICSSGIMNSPPICOCKLDFKSMKEGDYNPFIPIVAVMTAFSGLAFTIWLARLKK 360
      314 TICSSGIMNSPPICOCKLDFKSMKEGDYNPFIPIVAVMTAFSGLAFTIWLARLKK 373
      361 GKSKRSMNDPY 372
      374 GKSKRSMNDPY 385

RESULT 4
US-08-461-592B-2
; Sequence 2, Application US/08461592B
; Patent No. 5834425
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; APPLICANT: Kansas, Geoffrey S.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
; TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welngarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,592B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/340,539
; FILING DATE: 16-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,459
; FILING DATE: 25-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: CG-104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-592B-2
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Query Match      98.1%; Score 2076; DB 2; Length 385;
Best Local Similarity 98.1%; Pred. No. 1.3e-181;
Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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      61 YTDLVAIONKAEIEYLEKTLPEFSRSYIWKIRKIGITWTWGTNKSLTLEAENKGDSEPN 120
      74 YTDLVAIONKAEIEYLEKTLPEFSRSYIWKIRKIGITWTWGTNKSLTLEAENKGDSEPN 133
      121 NKKNEDECEVEIYIKRNKDAGKNDACCHKLKAALCYTASCPWSCSGHGEVEIINNHTC 180
      134 NKKNEDECEVEIYIKRNKDAGKNDACCHKLKAALCYTASCPWSCSGHGEVEIINNHTC 193
      181 NCDVGYGPOCQVYIOCEPLAPDLGIMNCSHPLASFSTACTPICSSEGTLLGIEETT 240
      194 NCDVGYGPOCQVYIOCEPLAPDLGIMNCSHPLASFSTACTPICSSEGTLLGIEETT 253
      241 CGPFGNWSPEPTCQVYIOCEPLAPDLGIMNCSHPLASFSTACTPICSSEGTLLGIEETT 300
      254 CGPFGNWSPEPTCQVYIOCEPLAPDLGIMNCSHPLASFSTACTPICSSEGTLLGIEETT 313
      301 TICSSGIMNSPPICOCKLDFKSMKEGDYNPFIPIVAVMTAFSGLAFTIWLARLKK 360
      314 TICSSGIMNSPPICOCKLDFKSMKEGDYNPFIPIVAVMTAFSGLAFTIWLARLKK 373
      361 GKSKRSMNDPY 372
      374 GKSKRSMNDPY 385

RESULT 5
US-08-513-278-4
; Sequence 4, Application US/08513278
; Patent No. 5840844
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: STACHELL, SCOTT E.
; APPLICANT: ROSEN, STEVEN D.
; APPLICANT: SINGER, MARK S.
; APPLICANT: YEDNICK, TED A.
; TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,278
; FILING DATE: 10-AUG-1995
; CLASSIFICATION: 5530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/059027
; FILING DATE: 06-MAY-1993
; APPLICATION NUMBER: 07/786149
; FILING DATE: 31-OCT-1991
; PRIOR APPLICATION DATA: 07/315015
; APPLICATION NUMBER: 07/315015
; FILING DATE: 23-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 565D1C1
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Query Match	78.0%;	Score 1651;	DB 6;	Length 372;
Best Local Similarity	76.1%;	Pred. No. 7.6e-143;		
Matches 283;	Conservative 32;	Mismatches 57;	Indels 0;	Gaps 0;

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1      RESULT 7
2      US-08-110-158-4
3      : Sequence 4, Application US/08110158
4      : Patent No. 5605821
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: McEvel, Rodger P.
9      :
10     : APPLICANT: Pan, Junliang
11     :
12     : TITLE OF INVENTION: Expression Control Sequences of the
13     :
14     : TITLE OF INVENTION: P-Selectin Gene
15     :
16     : NUMBER OF SEQUENCES: 17
17     :
18     : CORRESPONDENCE ADDRESS:
19     :
20     : ADDRESSEE: Patrea L. Pabst
21     :
22     : STREET: 1100 Peachtree Street, Suite 2800
23     :
24     : CITY: Atlanta
25     :
26     : STATE: GA
27     :
28     : COUNTRY: USA
29     :
30     : ZIP: 30309-4530
31     :
32     : COMPUTER READABLE FORM:
33     :
34     : MEDIUM TYPE: Floppy disk
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36     : COMPUTER: IBM PC compatible
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38     : OPERATING SYSTEM: PC-DOS/MS-DOS
39     :
40     : SOFTWARE: Patent Release #1.0, Version #1.25
41     :
42     : CURRENT APPLICATION DATA:
43     :
44     : APPLICATION NUMBER: US/08/110,158
45     :
46     : FILING DATE: 19930820
47     :
48     : CLASSIFICATION: 424
49     :
50     : PRIOR APPLICATION DATA:
51     :
52     : APPLICATION NUMBER: US 07/320,408
53     :
54     : FILING DATE: 08-MAR-1989
55     :
56     : ATTORNEY/AGENT INFORMATION:
57     :
58     : NAME: Pabst, Patrea L.
59     :
60     : REGISTRATION NUMBER: 31,284
61     :
62     : TELECOMMUNICATION INFORMATION:
63     :
64     : TELEPHONE: (404)-815-6508
65     :
66     : TELEFAX: (404)-815-6555
67     :
68     : INFORMATION FOR SEQ ID NO: 4:
69     :
70     : SEQUENCE CHARACTERISTICS:
71     :
72     : LENGTH: 830 amino acids
73     :
74     : TYPE: amino acid
75     :
76     : STRANDEDNESS: single
77     :
78     : TOPOLOGY: linear
79     :
80     : MOLECULE TYPE: peptide
81     :
82     : US-08-110-158-4

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? OTHER INFORMATION: /note= "Potential asparagine-linked
? OTHER INFORMATION: glycosylation site"
?
? FEATURE:
? NAME/KEY: Binding-site
? LOCATION: 665
? OTHER INFORMATION: /note= "Potential asparagine-linked
? OTHER INFORMATION: glycosylation site"
?
? FEATURE:
? NAME/KEY: Binding-site
? LOCATION: 716
? OTHER INFORMATION: /note= "Potential asparagine-linked
? OTHER INFORMATION: glycosylation site"
?
? FEATURE:

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Query Match	42.5%;	Score 899;	DB 5;	Length 830;
Best Local Similarity	50.3%;	Pred. No. 8.7e-74;		
Matches 156;	Conservative 48;	Mismatches 106;	Indels	

[illegible]

RESULT 9
5378464-2
Patent No. 5378464
APPLICANT: MCEYER, RODGER P.
TITLE OF INVENTION: MODULATION OF INFLAMMATORY RESPONSES
BY ADMINISTRATION OF GMP-140 OR ANTIBODY TO GMP-140
NUMBER OF SEQUENCES: 32
CURRENT APPLICATION NUMBER: 08-07/320,408
FILING DATE: 08-MAR-1989
SEQ ID NO.: 2
LENGTH: 830
5378464-2

	Query Match	42.0%	Score 889	DB 6	Length 830
	Best Local Similarity	50.0%	Pred. No. 7.1e-73		
	Matches 155	Conservative 48	Mismatches 107	Indels 0	Gaps 0
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		: : : : : : : : : :			
DB	11	QRFQRYVGEISOLCFSSALISLTYNOKEYAAWYTHYSTRFAVSWNISRKYCOMRYDVAI	70		
QY	68	ONKAEIIELEKTLPEFSRSYTWIGIRKIGIIMWTVSTNKSLEAEAMWDCDEPNKKNKED	127		
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DB	71	QNKNEIDILNKLPRYSYTWIGIRKNNKTYWTVSTKKAITNEALNADNEPNKRNKED	130		
QY	128	CVEIYIKRNKDGAKWNDACHKLKALCYTASCPWSCSGHGECVEIYINNHTCNDGVY	187		
DB	131	CVEIYIKSPSPAGKNNDMCKLKKALCYTASCOMSSGSGECLETIGNTGCTSPGFY	190		

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Oy 188 GPGCOLVQCEPLEAPELGTMDCTHPGNEFSFSQCAFSQSEGNLNLGIBETTCGPRGNM 247
Db 191 GPECYVECEBELLPOCVLWLNKSHPLGNSQSCSFHCTDGTQVWGPNSKLECLASGIW 250
Oy 248 SPSPECTCIVICEPLSAPDLGIMNCSPHLSFSTACTFICSGYGTGLGKKTKICSSG 307
Db 251 TNKPQCLAAQCPPLKIPERBNMTCMSAKRPQWQSSCSFCEGDFALVGEVYQCTASG 310
Oy 308 TWSNDSPICQ 317
Db 311 VMTAPAPVCK 320

RESULT 10
US-08-365-470-3
: Sequence 3, Application US/08365470
: Patent No. 5632991
: GENERAL INFORMATION:
: APPLICANT: Gimbrone, Jr., Michael A.
: TITLE OF INVENTION: Antibodies Specific For E-selectin And The Uses
: TITLE OF INVENTION: Thereof
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX
: STREET: 1100 New York Ave., NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/365,470
: FILING DATE: herewith
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/102,510
: FILING DATE: 05-AUG-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/850,802
: FILING DATE: 13-MAR-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Markowicz, Karen R.
: REGISTRATION NUMBER: 36,351
: REFERENCE/DOCKET NUMBER: 0627.1350003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 610 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-08-365-470-3

Query Match 40.7%; Score 862; DB 1; Length 610;
Best Local Similarity 52.0%; Pred. No. 1.4e-70;
Matches 145; Conservative 41; Mismatches 93; Indels 0; Gaps

Oy 39 WTYHYSEKPMWQARRFCRDNTYDVAIQKAEIYLEKTLPPSRSYWIGIRKIGIW 98
Db 22 WSYNTSTREAMYDEASAYACQQRTHLVAIQKEIEYLSITLSYSPSYWIGIRKVNWM 81

99 TWVGTSTNLSLEAENWMDGEBPNKKNKEDCYEYIKRKNKAGKKNDDACGKRLAALCYTA 158
Db 82 WVGQGRKRLTEAANKNMAPGEPPNNQKQKEDCYEYIKRKNKAGKKNDDACGKRLAALCYTA 141
Oy 159 SCQPMWSCGHECYEIIINNHCTNCVDGYGQCOLVQICEPLAPELGTMDCTHPGNGFS 218

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Query Match          40.7%; Score 862; DB 6; Length 610;

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;
; SEQ ID NO: 2
;
; LENGTH: 610
5217870-2

RESULT 12
5217870-2
; Patent No. 5217870
; APPLICANT: HESSION, CATHERINE A.; LOBB, ROY R.; GOELZ, SUSAN E.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST CDX
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/345,151
; FILING DATE: 28-APR-1989
; SEQ ID NO: 2
;
; LENGTH: 610
5217870-2

Query Match          40.7%; Score 862; DB 6; Length 610;

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;
; SEQ ID NO: 2
;
; LENGTH: 610
5217870-2

RESULT 11
US-09-209-668-19
; Sequence 19, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 610
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-209-668-19

Query Match          40.7%; Score 862; DB 3; Length 610;
Best Local Similarity 52.0%; Pred. NO.1.4e-70;
Matches 145; Conservative 41; Mismatches 93; Indels 0; Gaps 0.

QY 39 WTYHYSEKPMNQARRRCRDNYTDLVALIIONKAEILEYLEKTLFSSRSYYWIGIRKIGIW 98
D 22 WSYNSTEAMTYDEASAYCQQRHYTHLVAIONKEIEYILNSILSPSYWIGIRKYNWV 81
QY 99 TWVGINKSLTEBAEWGCGEPNNKKNKEDCVETIYIKRNKDAGKWNDDACHIKALACTYA 158
D 82 VVWGQKPLTEAKKMAWGEPPNNRQKDDCVETIYIKREDVGMWMDERCSKKKALACTYA 141
QY 159 SCQPMSCSGHGHCVEIINNNHCNCNDGVYGGPCQCLVIOCEPLEAEDELGTMDCTHPFGNFS 218
D 142 ACTNNTSCSGHGECVETIINNYYTCKDPCPGFSGLKCEQIVNCTALESPHSGSLVCSHPLGNFS 201
QY 219 FSSQCAFSCSEGTNLGTLEETTCGPFGMWSSPEPTCOVIOCEPLSAPDGLGIMNCSHPLAS 278
D 202 YNNSCSISCDRGYLPSSMETMQCMSSGEMSAPIPACNVVECDVAVNPANGFVECFQNPGS 261
QY 279 FSTISACFFICSEGTLELIGKKKTTIESSGIMSNPSPICQ 317
D 262 FPMWNTTCFDECEGFEELMGAQSLQCTSGMNDNEKPTCK 300

RESULT 11
US-09-209-668-19
; Sequence 19, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 610
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-209-668-19

Query Match          40.7%; Score 862; DB 6; Length 610;

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;
; SEQ ID NO: 2
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; LENGTH: 610
5217870-2

RESULT 12
5217870-2
; Patent No. 5217870
; APPLICANT: HESSION, CATHERINE A.; LOBB, ROY R.; GOELZ, SUSAN E.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST CDX
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/345,151
; FILING DATE: 28-APR-1989
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; LENGTH: 610
5217870-2

Query Match          40.7%; Score 862; DB 6; Length 610;

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; LENGTH: 610
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RESULT 11
US-09-209-668-19
; Sequence 19, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Homo sapiens
US-09-209-668-19

Query Match          40.7%; Score 862; DB 3; Length 610;
Best Local Similarity 52.0%; Pred. NO.1.4e-70;
Matches 145; Conservative 41; Mismatches 93; Indels 0; Gaps 0.

QY 39 WTYHYSEKPMNQARRRCRDNYTDLVALIIONKAEILEYLEKTLFSSRSYYWIGIRKIGIW 98
D 22 WSYNSTEAMTYDEASAYCQQRHYTHLVAIONKEIEYILNSILSPSYWIGIRKYNWV 81
QY 99 TWVGINKSLTEBAEWGCGEPNNKKNKEDCVETIYIKRNKDAGKWNDDACHIKALACTYA 158
D 82 VVWGQKPLTEAKKMAWGEPPNNRQKDDCVETIYIKREDVGMWMDERCSKKKALACTYA 141
QY 159 SCQPMSCSGHGHCVEIINNNHCNCNDGVYGGPCQCLVIOCEPLEAEDELGTMDCTHPFGNFS 218
D 142 ACTNNTSCSGHGECVETIINNYYTCKDPCPGFSGLKCEQIVNCTALESPHSGSLVCSHPLGNFS 201
QY 219 FSSQCAFSCSEGTNLGTLEETTCGPFGMWSSPEPTCOVIOCEPLSAPDGLGIMNCSHPLAS 278
D 202 YNNSCSISCDRGYLPSSMETMQCMSSGEMSAPIPACNVVECDVAVNPANGFVECFQNPGS 261
QY 279 FSTISACFFICSEGTLELIGKKKTTIESSGIMSNPSPICQ 317
D 262 FPMWNTTCFDECEGFEELMGAQSLQCTSGMNDNEKPTCK 300

RESULT 11
US-09-209-668-19
; Sequence 19, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
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; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-209-668-19

Query Match          40.7%; Score 862; DB 6; Length 610;

;
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5217870-2

RESULT 12
5217870-2
; Patent No. 5217870
; APPLICANT: HESSION, CATHERINE A.; LOBB, ROY R.; GOELZ, SUSAN E.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST CDX
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/345,151
; FILING DATE: 28-APR-1989
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; LENGTH: 610
5217870-2

Query Match          40.7%; Score 862; DB 6; Length 610;

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; LENGTH: 610
5217870-2

RESULT 11
US-09-209-668-19
; Sequence 19, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 610
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-209-668-19

Query Match          40.7%; Score 862; DB 3; Length 610;
Best Local Similarity 52.0%; Pred. NO.1.4e-70;
Matches 145; Conservative 41; Mismatches 93; Indels 0; Gaps 0.

QY 39 WTYHYSEKPMNQARRRCRDNYTDLVALIIONKAEILEYLEKTLFSSRSYYWIGIRKIGIW 98
D 22 WSYNSTEAMTYDEASAYCQQRHYTHLVAIONKEIEYILNSILSPSYWIGIRKYNWV 81
QY 99 TWVGINKSLTEBAEWGCGEPNNKKNKEDCVETIYIKRNKDAGKWNDDACHIKALACTYA 158
D 82 VVWGQKPLTEAKKMAWGEPPNNRQKDDCVETIYIKREDVGMWMDERCSKKKALACTYA 141
QY 159 SCQPMSCSGHGHCVEIINNNHCNCNDGVYGGPCQCLVIOCEPLEAEDELGTMDCTHPFGNFS 218
D 142 ACTNNTSCSGHGECVETIINNYYTCKDPCPGFSGLKCEQIVNCTALESPHSGSLVCSHPLGNFS 201
QY 219 FSSQCAFSCSEGTNLGTLEETTCGPFGMWSSPEPTCOVIOCEPLSAPDGLGIMNCSHPLAS 278
D 202 YNNSCSISCDRGYLPSSMETMQCMSSGEMSAPIPACNVVECDVAVNPANGFVECFQNPGS 261
QY 279 FSTISACFFICSEGTLELIGKKKTTIESSGIMSNPSPICQ 317
D 262 FPMWNTTCFDECEGFEELMGAQSLQCTSGMNDNEKPTCK 300

RESULT 11
US-09-209-668-19
; Sequence 19, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 610
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-209-668-19

Query Match          40.7%; Score 862; DB 6; Length 610;

;
;
; SEQ ID NO: 2
;
; LENGTH: 610
5217870-2

RESULT 12
5217870-2
; Patent No. 5217870
; APPLICANT: HESSION, CATHERINE A.; LOBB, ROY R.; GOELZ, SUSAN E.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST CDX
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/345,151
; FILING DATE: 28-APR-1989
; SEQ ID NO: 2
;
; LENGTH: 610
5217870-2

Query Match          40.7%; Score 862; DB 6; Length 610;

;
;
; SEQ ID NO: 2
;
; LENGTH: 610
5217870-2

RESULT 11
US-09-209-668-19
; Sequence 19, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 6
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Best Local Similarity 52.0%; Pred. No. 1.4e-70;
Matches 145; Conservative 41; Mismatches 93; Indels 0; Gaps 0;

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QY 39 WTHYSEKPNMORARFCRDNTDLVAIONKAEIYLELTPSRSYWIGIRKIGTW 98
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 WSYTSTSEATWTFDASAYVCOQRYTHLVAIONKAEIYLELSTFNSYASWIGIRKINGTW 81
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
QY 99 TWGTSKSLTELEANNMGDGPNNKKNEKDCVEIYIRKNDAGKWNDDACHKLKALCYTA 158
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 VWMGTOKPLTELEAKNMAKGPNNRQKDEDCVEIYIRKNDAGKWNDDACHKLKALCYTA 141
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
QY 159 SCOPWSCSGHGECEVEIINHTCNCVGYGPOCOLYIOCEPLAPDLGIMNCSHPLAS 218
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 ACTNTSCSGHGECEVEIINHTCNCVGYGPOCOLYIOCEPLAPDLGIMNCSHPLAS 201
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
QY 219 FSSQCAFSCSGEVEIINHTCNCVGYGPOCOLYIOCEPLAPDLGIMNCSHPLAS 278
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 YNSSCSISCRGYPSSMETMOCSSGEMWAPIPACNVCDCDAVTNPANGFVECFQNPBS 261
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
QY 279 FSFTSACTFICSEGTTELIGKKTICSSGIMSNPSPICO 317
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 262 FPMNTCTFDCBEGFELMGASIQCTISSGWNDEKPTCK 300
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RESULT 13

US-08-252-493C-9
Sequence 9, Application US/08252493C
Patent No. 5891645

GENERAL INFORMATION:

APPLICANT: Rollins, Scott
APPLICANT: Rother, Russell P.
APPLICANT: Evans, Mark J.
APPLICANT: Matis, Louis A.
TITLE OF INVENTION: PORCINE E-SELECTIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel
STREET: 25 Science Park, Box 15
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06511

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 750 Kb storage
COMPUTER: PC compatible
OPERATING SYSTEM: DOS 6.2
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,493C
FILING DATE: June 1, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449

TELECOMMUNICATION INFORMATION:

TELEPHONE: (203) 776-1790
TELEFAX: (203) 772-3655
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

LENGTH: 484 amino acids

TYPE: amino acid

STRANDEDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: cDNA to mRNA

DESCRIPTION: Predicted amino acid sequence of

TELECOMMUNICATION INFORMATION:

US-08-252-493C-9

Query Match 38.5%; Score 814.5; DB 2; Length 484;
Best Local Similarity 36.1%; Pred. No. 2.2e-66;
Matches 159; Conservative 55; Mismatches 109; Indels 117; Gaps 7;

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QY 39 WTHYSEKPNMORARFCRDNTDLVAIONKAEIYLELTPSRSYWIGIRKIGTW 98
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 23 WSYTSTSEATWTFDASAYVCOQRYTHLVAIONKAEIYLELSTFNSYASWIGIRKINGTW 82
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
QY 99 TWGTSKSLTELEANNMGDGPNNKKNEKDCVEIYIRKNDAGKWNDDACHKLKALCYTA 158
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 TWIGTKALTPLEATNMAKGPNNRQKDEDCVEIYIRKNDAGKWNDDACHKLKALCYTA 142
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
QY 159 SCOPWSCSGHGECEVEIINHTCNCVGYGPOCOLYIOCEPLAPDLGIMNCSHPLAS 211
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 143 ACTPTSCSGHGECEVEIINHTCNCVGYGPOCOLYIOCEPLAPDLGIMNCSHPLAS 202
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
QY 212 -----HP-----FGNFS 218
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 203 TCAPFCKEFGELIGPBLQCTSSGSDGKKPTCKAVTCDTVGHPQGDVSCNHSSTGEPA 262
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
QY 219 FSSQCAFSCSGEVEIINHTCNCVGYGPOCOLYIOCEPLAPDLGIMNCSHPLA 277
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 263 YKSTCHFTCAEGFGIOPAIIECTAGOGWTQAPVCRAKCAVSPKKNLKFTHSPG 322
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
QY 278 FSFTSACTFICSEGTTELIGKKTICSSGIMSNPSPICO-----KDKSFSMTKEGD 330
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 323 EFTYKSCAFSCBEGFELNGSAQLACTSOGQWTVQEPSCQVYQCSLEVPREINMSCSGE 382
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
QY 331 YNPLF-----IPAVAVTA----- 344
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 383 --PVFQAVCTFACPEGMMLNGSVALTCGATGWSGLPTCEAPAESKIPLAMGLAAGVS 440
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QY 345 -FSGLAFTIIMARLKKKK 363
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 441 FMTSASFLLMLKRLKRAK 460
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 14

US-09-276-197-9
Sequence 9, Application US/09276197
Patent No. 6040428

GENERAL INFORMATION:

APPLICANT: Rollins, Scott
APPLICANT: Rother, Russell P.
APPLICANT: Evans, Mark J.
APPLICANT: Matis, Louis A.
TITLE OF INVENTION: PORCINE E-SELECTIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel
STREET: 25 Science Park, Box 15
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06511

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 750 Kb storage
COMPUTER: PC compatible
OPERATING SYSTEM: DOS 6.2
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,197
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/252,493

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449

TELECOMMUNICATION INFORMATION:

TELEPHONE: (203) 776-1790


```

; TELEFAX: (203) 772-3655
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 484 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; DESCRIPTION: predicted amino acid sequence of
; DESCRIPTION: Porcine E-selectin
; US-09-276-197-9

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Query Match      38.5%; Score 814.5; DB 3; Length 484;
Best Local Similarity 36.1%; Pred. No. 2.2e-66;
Matches 159; Conservative 55; Mismatches 109; Indels 117; Gaps 7;

```

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QY 39 WTYHYSEKPMNMORARRFCRDNYTDLVAIONKAEIYLEKTLPPSRSYWIGIRKIGIW 98
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 23 WSYTSASTETMTFPDDASAYCQQRTHLVAIONHAEIETLNTSTFKTSASYWIGIRKIGIW 82

QY 99 TWVGTNKSLEAEENWGDGEPPNNKKNKEDCEVEIYIKRNKDGKWNDDACHKLKALCYTA 158
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 83 TWIGTKKALPPEATNMAPGEPNNKQSNEDCEVEIYIKRDKSGKWNDRCSKKLALCYTA 142

QY 159 SCQPMWSSGSGEVEITNNHTCNDVGYVGPQCQLVQCEPLEPELGTMDC----- 211
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 143 ACPTSCSGHGECIETINSSTCOCYPGFRIGICEQVVECDALNPVGVYTCQPSLPMWT 202

QY 212 -----HP-----FQNFSS 218
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 203 TCAPECKEFGELIGPEHLOCTSSGSMWDGKKPTCAVTCDPVGHQNDVDVSCNHSSTIEFA 262

QY 219 FSSQCAFCSEGTNLGIEETTCGPFQGNWSSPEPTCQVIOCEPLSADLGMNCSH-PLA 277
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 263 YKSTCHFTCAEGFGLQGPQIETAGOGWTOQAAPVCAKAVCPAASQPKNGLVKFTHSPTG 322

QY 278 SFPTSACTFTICSEGTFLIKKKTICSSSISWNPSPICQ-----KLDKSPSMIEGD 330
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 323 EFTYKSSCAFSCEGFEELRGSADLACTSGQWTOEVPSCQVOCSSLEVPREIMSCSG 382

QY 331 YNPLF-----IPAVVMVTA----- 344
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 383 --PVFGAVCTFACPEGMLNGSVALTGCGATGHSGLPFCPEAPAESKIPFLAMGLAAGVS 440

QY 345 -FSGLAFTIWLARRLKKKK 363
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Db 441 FMTSASFLLWLKRLKRRAK 460

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```

RESULT 15
US-08-274-661B-38
; Sequence 38, Application US/08274661B
; Patent No. 5593882
; GENERAL INFORMATION:
;   APPLICANT: Erbe, David V.
;   APPLICANT: Lasky, Laurence A.
;   APPLICANT: Presta, Leonard G.
;   TITLE OF INVENTION: Selectin Variants
;   NUMBER OF SEQUENCES: 39
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 460 Point San Bruno Blvd
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatIn (Genentech)
;   CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/274,661B
; FILING DATE: 13-Jul-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/956701
;   FILING DATE: 10/01/1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Dreger, Ginger R.
;     REGISTRATION NUMBER: 33,055
;     REFERENCE/DOCKET NUMBER: 761P1C1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415/225-3216
;   TELEFAX: 415/952-9881
;   TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 117 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
; US-08-274-661B-38

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Query Match      31.5%; Score 666; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.2e-53;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 39 WTYHYSEKPMNMORARRFCRDNYTDLVAIONKAEIYLEKTLPPSRSYWIGIRKIGIW 98
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 WTYHYSEKPMNMORARRFCRDNYTDLVAIONKAEIYLEKTLPPSRSYWIGIRKIGIW 60

QY 99 TWVGTNKSLEAEENWGDGEPPNNKKNKEDCEVEIYIKRNKDGKWNDDACHKLKALC 155
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 TWVGTNKSLEAEENWGDGEPPNNKKNKEDCEVEIYIKRNKDGKWNDDACHKLKALC 117

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Search completed: October 13, 2001, 02:55:41
Job time: 719 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2001, 02:48:44 ; Search time 164.14 Seconds

(Without alignments)
502.786 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116
Sequence: 1 MIFPMKCOSTGRDLMNIFKL.....WLARRLKGGKSKSRMNDPY 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues

Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_Main:*

1: /cgnl_7/ptodata/1/paa/US06_COMB.pep:*
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23: /cgnl_7/ptodata/1/paa/US09_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2116	100.0	372	15	US-09-119-209-2
2	2076	98.1	385	1	PCT-US92-03970-2
3	2076	98.1	385	1	PCT-US94-00909-2
4	2076	98.1	385	4	US-08-008-459-2
5	2076	98.1	385	7	US-08-340-539-2
6	2076	98.1	385	8	US-08-410-569-2
7	1883	89.0	1078	23	US-60-212-659-523
8	1879	88.8	1078	23	US-60-207-315-428
9	1879	88.8	1078	23	US-60-230-435-1751
10	1651	78.0	372	15	US-09-119-209-4

11	905	42.8	830	1	PCT-US94-09395-4	Sequence 4, Appl1
12	905	42.8 <td>830</td> <td>8</td> <td>US-08-449-6878-4</td> <td>Sequence 4, Appl1</td>	830	8	US-08-449-6878-4	Sequence 4, Appl1
13	898	42.4	700	23	US-60-207-315-467	Sequence 467, App
14	862	40.7	610	1	PCT-US99-28965-19	Sequence 19, Appl
15	862	40.7	610	10	US-08-657-753-2	Sequence 2, Appl1
16	862	40.7	610	11	US-08-770-435-3	Sequence 3, Appl1
17	862	40.7	610	14	US-09-009-490A-89	Sequence 89, Appl1
18	862	40.7	610	16	US-09-266-091A-2	Sequence 2, Appl1
19	862	40.7	610	16	US-09-266-091A-2	Sequence 2, Appl1
20	862	40.7	610	22	US-09-802-640-36	Sequence 36, Appl
21	666	31.5	119	23	US-60-160-189-8687	Sequence 8687, Ap
22	666	31.5	119	23	US-60-169-867-5823	Sequence 5823, Ap
23	645	30.5	119	23	US-60-160-203-5003	Sequence 5003, Ap
24	645	30.5	119	23	US-60-169-840-6716	Sequence 6716, Ap
25	586	27.7	116	23	US-60-160-189-10011	Sequence 10011, A
26	586	27.7	116	23	US-60-160-203-6200	Sequence 6200, Ap
27	586	27.7	116	23	US-60-169-840-9336	Sequence 9336, Ap
28	586	27.7	116	23	US-60-169-867-7998	Sequence 7998, Ap
29	452.5	21.4	129	23	US-60-196-718-4236	Sequence 4236, Ap
30	451.5	21.3	129	23	US-60-195-053-1909	Sequence 1909, Ap
31	451.5	21.3	129	23	US-60-195-053-1908	Sequence 1908, Ap
32	451.5	21.3	138	23	US-60-196-718-4238	Sequence 4238, Ap
33	447.5	21.1	132	23	US-60-196-718-4237	Sequence 4237, Ap
34	416	19.7	112	23	US-60-160-203-3503	Sequence 3503, Ap
35	415.5	19.6	130	23	US-60-196-174-903	Sequence 903, App
36	415	19.6	134	23	US-60-192-739-3226	Sequence 3226, Ap
37	403	19.0	104	23	US-60-160-189-5792	Sequence 5792, Ap
38	389	18.4	115	23	US-60-196-718-3944	Sequence 3944, Ap
39	388	18.3	68	23	US-60-163-123-1859	Sequence 1859, Ap
40	388	18.3	68	23	US-60-163-123-1859	Sequence 1859, Ap
41	283.5	13.4	355	1	PCT-US01-01332-615	Sequence 615, App
42	266	12.6	309	1	PCT-US01-01332-615	Sequence 615, App
43	254	12.0	75	23	US-60-188-162-5010	Sequence 5010, Ap
44	248	11.7	135	23	US-60-196-718-4486	Sequence 4486, Ap
45	247.5	11.7	1124	23	US-60-191-637-1341	Sequence 1341, Ap

ALIGNMENTS

RESULT 1
US-09-119-209-2
GENERAL INFORMATION: Application US/09119209
APPLICANT: LASTY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: YEDNICK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
City: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,209
FILING DATE: 20-Jul-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513278
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059027
FILING DATE: 6-MAY-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/315015
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0565DLIC3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
US-09-119-209-2

Query Match 100.0%; Score 2116; DB 15; Length 372;
Best Local Similarity 100.0%; Pred. No. 7.6e-177;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPMKQSTORDLWNIIFKLMGWTMLCCDFLAHGGTYCWTYHSEKPMNQARARFCRDN 60
DB 1 MIFPMKQSTORDLWNIIFKLMGWTMLCCDFLAHGGTYCWTYHSEKPMNQARARFCRDN 60
QY 61 YTDVLAIONKAEIELEKTLPEFSRSYTWIGIRKIGITWTWGTNKSITLFEAENMGDEPN 120
DB 61 YTDVLAIONKAEIELEKTLPEFSRSYTWIGIRKIGITWTWGTNKSITLFEAENMGDEPN 120
QY 121 NKKNKEDCEYIYIKRNKDGKWNDDACHKLAALCYTASCPWSCSGHGECEVEIINNHTC 180
DB 121 NKKNKEDCEYIYIKRNKDGKWNDDACHKLAALCYTASCPWSCSGHGECEVEIINNHTC 180
QY 181 NCDVGYGPOCQVIOCEPLAEPDLGTMCTHPHGFNSFSSQCAFSCSGTNLGIEETT 240
DB 181 NCDVGYGPOCQVIOCEPLAEPDLGTMCTHPHGFNSFSSQCAFSCSGTNLGIEETT 240
QY 241 CGPFGNWSPEPTQVIOCEPLAEPDLGIMNCSHPLASFSTSACTFICSEGTLLGKKK 300
DB 241 CGPFGNWSPEPTQVIOCEPLAEPDLGIMNCSHPLASFSTSACTFICSEGTLLGKKK 300
QY 301 TICSSGIMSNPSPIQKLDKSFMSIKEGDYNPLFIPIAVVMTAFSGIAFIIMLARLKK 360
DB 301 TICSSGIMSNPSPIQKLDKSFMSIKEGDYNPLFIPIAVVMTAFSGIAFIIMLARLKK 360
QY 361 GKSKRSNMNDPY 372
DB 361 GKSKRSNMNDPY 372

RESULT 2
PCT-US92-03970-2

Sequence 2, Application PC/TUS9203970
GENERAL INFORMATION:
APPLICANT: Dana-Farber Cancer Institute, Inc.
TITLE OF INVENTION: LEUKOCYTE-ASSOCIATED CELL SURFACE
NUMBER OF INVENTIONS: PROTEIN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03970
FILING DATE: 19920513
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Heine, Holliday C.
REGISTRATION NUMBER: DFCI-152Bq9
REFERENCE/DOCKET NUMBER: DFCI-152Bq9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-03970-2

Query Match 98.1%; Score 2076; DB 1; Length 385;
Best Local Similarity 98.1%; Pred. No. 2.6e-173;

Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIFPMKQSTORDLWNIIFKLMGWTMLCCDFLAHGGTYCWTYHSEKPMNQARARFCRDN 60
DB 14 MIFPMKQSTORDLWNIIFKLMGWTMLCCDFLAHGGTYCWTYHSEKPMNQARARFCRDN 73
QY 61 YTDVLAIONKAEIELEKTLPEFSRSYTWIGIRKIGITWTWGTNKSITLFEAENMGDEPN 120
DB 74 YTDVLAIONKAEIELEKTLPEFSRSYTWIGIRKIGITWTWGTNKSITLFEAENMGDEPN 133
QY 121 NKKNKEDCEYIYIKRNKDGKWNDDACHKLAALCYTASCPWSCSGHGECEVEIINNHTC 180
DB 134 NKKNKEDCEYIYIKRNKDGKWNDDACHKLAALCYTASCPWSCSGHGECEVEIINNHTC 193
QY 181 NCDVGYGPOCQVIOCEPLAEPDLGTMCTHPHGFNSFSSQCAFSCSGTNLGIEETT 240
DB 194 NCDVGYGPOCQVIOCEPLAEPDLGTMCTHPHGFNSFSSQCAFSCSGTNLGIEETT 253
QY 241 CGPFGNWSPEPTQVIOCEPLAEPDLGIMNCSHPLASFSTSACTFICSEGTLLGKKK 300
DB 254 CGPFGNWSPEPTQVIOCEPLAEPDLGIMNCSHPLASFSTSACTFICSEGTLLGKKK 313
QY 301 TICSSGIMSNPSPIQKLDKSFMSIKEGDYNPLFIPIAVVMTAFSGIAFIIMLARLKK 360
DB 314 TICSSGIMSNPSPIQKLDKSFMSIKEGDYNPLFIPIAVVMTAFSGIAFIIMLARLKK 373
QY 361 GKSKRSNMNDPY 372
DB 374 GKSKRSNMNDPY 385

RESULT 3
PCT-US94-00909-2

Sequence 2, Application PC/TUS9400909
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS BLOCKING
NUMBER OF INVENTIONS: AGENTS FOR COMPONENT SELECTIN FUNCTION
NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00909
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,606
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/962,483
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,608
; FILING DATE: 03-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/737,092
; FILING DATE: 29-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/730,503
; FILING DATE: 08-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/700,773
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/313,109
; FILING DATE: 21-FEB-1989
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-00909-2

```

Query Match 98.1%; Score 2076; DB 1; Length 385;

Best Local Similarity 98.1%; Pred. No. 2.6e-173; Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MIFPMKQSTORDLWNIIFKLMGWTMLCCDFLAHHGTYCWTYHSEKPMNQARARFCRDN 60
DB 14 MIFPMKQSTORDLWNIIFKLMGWTMLCCDFLAHHGTYCWTYHSEKPMNQARARFCRDN 73
QY 61 YTDLVAIQNKAIEYLEKTLPFSSRYWIGIRKIGIWTWVGTKSLTEBAENMGDEPN 120
DB 74 YTDLVAIQNKAIEYLEKTLPFSSRYWIGIRKIGIWTWVGTKSLTEBAENMGDEPN 133
QY 121 NKKNKEDCEVIYIKRNKDAGKWDNDACHKIKALCYTASQPMSCSGHGCVEIINNHTC 180
DB 134 NKKNKEDCEVIYIKRNKDAGKWDNDACHKIKALCYTASQPMSCSGHGCVEIINNHTC 193
QY 181 NCDVGYGPOCOVIOCEPLEAPELGTMCTHPFGNFSFSSQCAFSCSEGTNLGIEETT 240
DB 194 NCDVGYGPOCOVIOCEPLEAPELGTMCTHPFGNFSFSSQCAFSCSEGTNLGIEETT 253
QY 241 CGPFGMWSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFESFTSACTFTICSEGTNLGIE 300
DB 254 CGPFGMWSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFESFTSACTFTICSEGTNLGIE 313
QY 301 TICSEGGINSNPPTIOKLDKSFMSIKEGDYNLFIPVAVMTAFSGLATIIMLARLKK 360
DB 314 TICSEGGINSNPPTIOKLDKSFMSIKEGDYNLFIPVAVMTAFSGLATIIMLARLKK 373
QY 361 GKSKRSMDPY 372
DB 374 GKSKRSMDPY 385

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```

RESULT 4
US-08-008-459-2
; Sequence 2, Application US/08008459
; GENERAL INFORMATION:
; APPLICANT: Teoder, Thomas F.
; APPLICANT: Kansas, Geoffrey S.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
; TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

```

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; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,459
; FILING DATE: 25-JAN-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,606
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,483
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,608
; FILING DATE: 03-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/737,092
; FILING DATE: 29-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/730,503
; FILING DATE: 08-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/700,773
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/313,109
; FILING DATE: 21-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Heine, Holliday C.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DFCI-318XX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; FAX: 940675
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-008-459-2

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Query Match 98.1%; Score 2076; DB 4; Length 385;

Best Local Similarity 98.1%; Pred. No. 2.6e-173; Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MIFPMKQSTORDLWNIIFKLMGWTMLCCDFLAHHGTYCWTYHSEKPMNQARARFCRDN 60
DB 14 MIFPMKQSTORDLWNIIFKLMGWTMLCCDFLAHHGTYCWTYHSEKPMNQARARFCRDN 73
QY 61 YTDLVAIQNKAIEYLEKTLPFSSRYWIGIRKIGIWTWVGTKSLTEBAENMGDEPN 120
DB 74 YTDLVAIQNKAIEYLEKTLPFSSRYWIGIRKIGIWTWVGTKSLTEBAENMGDEPN 133
QY 121 NKKNKEDCEVIYIKRNKDAGKWDNDACHKIKALCYTASQPMSCSGHGCVEIINNHTC 180
DB 134 NKKNKEDCEVIYIKRNKDAGKWDNDACHKIKALCYTASQPMSCSGHGCVEIINNHTC 193
QY 181 NCDVGYGPOCOVIOCEPLEAPELGTMCTHPFGNFSFSSQCAFSCSEGTNLGIEETT 240
DB 194 NCDVGYGPOCOVIOCEPLEAPELGTMCTHPFGNFSFSSQCAFSCSEGTNLGIEETT 253

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QY 241 CGPFGMWSPEPTCOVIOCEPLSAPDLGIMNCSPHLSAFTSACTFICSGTELGKK 300
DB 254 CEPFGMWSPEPTCOVIOCEPLSAPDLGIMNCSPHLSAFTSACTFICSGTELGKK 313
QY 301 TICESGIMSNPSPIQCKLDRKFSMIKEGDYNPLFIPAAVWTAFFSGIAFIIMLARLKK 360
DB 314 TICESGIMSNPSPIQCKLDRKFSMIKEGDYNPLFIPAAVWTAFFSGIAFIIMLARLKK 373
QY 361 GKSKRSMNDPY 372
DB 374 GKSKRSMNDPY 385

RESULT 5
US-08-340-539-2
; Sequence 2, Application US/08340539
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
; TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,539
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,459
; FILING DATE: 25-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,606
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,483
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,608
; FILING DATE: 03-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/737,092
; FILING DATE: 29-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/30,503
; FILING DATE: 08-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/700,773
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/313,109
; FILING DATE: 21-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Heine, Holliday C.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DFCI-318XX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2280
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids

QY 1 MIFPMKCOSTORDLNMIFKLMGWTMLCCDFLAHGGTCWTYHSKPMNMOBARRECCDN 60
DB 14 MIFPMKCOSTORDLNMIFKLMGWTMLCCDFLAHGGTCWTYHSKPMNMOBARRECCDN 73
QY 61 YIDLVAIONKAEILEYLEKTLFESRSYTWIGIRKIGIWTWGTNKSLEAEANWGDGEPN 120
DB 74 YIDLVAIONKAEILEYLEKTLFESRSYTWIGIRKIGIWTWGTNKSLEAEANWGDGEPN 133
QY 121 NKNKEDCWEIYIKRKDKGKNDACCHKLKALCYTASCCQWSCSGEGVEIINHTC 180
DB 134 NKNKEDCWEIYIKRKDKGKNDACCHKLKALCYTASCCQWSCSGEGVEIINHTC 193
QY 181 NCDVGYGPGCOLVIOCEPLSAPDLGIMNCSPHLSAFTSACTFICSGTELGKK 240
DB 194 NCDVGYGPGCOLVIOCEPLSAPDLGIMNCSPHLSAFTSACTFICSGTELGKK 253
QY 241 CGPFGMWSPEPTCOVIOCEPLSAPDLGIMNCSPHLSAFTSACTFICSGTELGKK 300
DB 254 CEPFGMWSPEPTCOVIOCEPLSAPDLGIMNCSPHLSAFTSACTFICSGTELGKK 313
QY 301 TICESGIMSNPSPIQCKLDRKFSMIKEGDYNPLFIPAAVWTAFFSGIAFIIMLARLKK 360
DB 314 TICESGIMSNPSPIQCKLDRKFSMIKEGDYNPLFIPAAVWTAFFSGIAFIIMLARLKK 373
QY 361 GKSKRSMNDPY 372
DB 374 GKSKRSMNDPY 385

Query Match 98.1%; Score 2076; DB 7; Length 385;
Best Local Similarity 98.1%; Pred. No. 2,6e-173;
Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-340-539-2

RESULT 6
US-08-410-569-2
; Sequence 2, Application US/08410569
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OF INVENTION: LEUKOCYTE ADHESION MOLECULE-1 (LAM-1)
; TITLE OF INVENTION: AND LIGAND THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,569
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,608
; FILING DATE: 03-OCT-1991
; APPLICATION NUMBER: US 07/700,773
; FILING DATE: 15-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heine, Holliday C.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DFCG-152EX

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
TELEX: 940675
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-410-569-2

Query Match 98.1%; Score 2076; DB 8; Length 385;
Best Local Similarity 98.1%; Pred. No. 2,6e-173;

Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIFPMKCGSTQRDLMNIFKLGWMTMLCCDFLAHHGTYCWTYHYSEKPMNQRRARFCRDN 60
DB 14 MIFPMKCGSTQRDLMNIFKLGWMTMLCCDFLAHHGTYCWTYHYSEKPMNQRRARFCRDN 73
QY 61 YTDVAIQNKAEIYLEKTLPEFSRSYYWIGIRKIGIMTWGINKSLTEBAENMGDEPN 120
DB 74 YTDVAIQNKAEIYLEKTLPEFSRSYYWIGIRKIGIMTWGINKSLTEBAENMGDEPN 133
QY 121 NKKNKEDCVETIYKRNKDKAGKMDACCHKIKALCYTASQCPMSSGSGHGCVELINNHTC 180
DB 134 NKKNKEDCVETIYKRNKDKAGKMDACCHKIKALCYTASQCPMSSGSGHGCVELINNHTC 193
QY 181 NCDVGYGPOCOLVIOCEPLEAPELGTMDCTHPGNFSFSSQCAFSCSEGTNLGIEETT 240
DB 194 NCDVGYGPOCOLVIOCEPLEAPELGTMDCTHPGNFSFSSQCAFSCSEGTNLGIEETT 253
QY 241 CGEFGMWSSEPTQYIOCEPLSAPDLGIMNCSHPLASFSTACTFICSEGTLLGKKK 300
DB 254 CGEFGMWSSEPTQYIOCEPLSAPDLGIMNCSHPLASFSTACTFICSEGTLLGKKK 313
QY 301 TICSESGINSPSPICQKLDKSFSAIKEGDYNLFIPVAVMTAFSGLAFTIILARLKK 360
DB 314 TICSESGINSPSPICQKLDKSFSAIKEGDYNLFIPVAVMTAFSGLAFTIILARLKK 373
QY 361 GKSKRSMDPY 372
DB 374 GKSKRSMDPY 385

RESULT 7

US-60-212-659-523
Sequence 523, Application US/60212659

GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
FILE REFERENCE: C1000674
CURRENT APPLICATION NUMBER: US/60/212,659
CURRENT FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 879
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 523
LENGTH: 1078
TYPE: PRT
ORGANISM: HUMAN
US-60-212-659-523

Query Match 89.0%; Score 1883; DB 23; Length 1078;
Best Local Similarity 97.4%; Pred. No. 7,8e-156;

Matches 336; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 22 GWTMLCCDFLAHHGTYCWTYHYSEKPMNQRRARFCRDNTDVAIQNKAEIYLEKTL 81
DB 604 GYFLPSKDFLAHHGTYCWTYHYSEKPMNQRRARFCRDNTDVAIQNKAEIYLEKTL 663

QY 82 FSRSYWIGIRKIGIMTWGINKSLTEBAENMGDEPNKKKNEKDCVEIYKRNKDGK 141
DB 664 FSRSYWIGIRKIGIMTWGINKSLTEBAENMGDEPNKKKNEKDCVEIYKRNKDGK 723
QY 142 WNDACHKRLKALCYTASCPMWSGSGHGCVEIINNHTCNDGVYGPQOLVIOCEPLE 201
DB 724 WNDACHKRLKALCYTASCPMWSGSGHGCVEIINNHTCNDGVYGPQOLVIOCEPLE 783
QY 202 APELGTMDCTHPGNFSFSSQCAFSCSEGTNLGIEETTCGPRGMSPEPTCOVIOCEP 261
DB 784 APELGTMDCTHPGNFSFSSQCAFSCSEGTNLGIEETTCGPRGMSPEPTCOVIOCEP 843
QY 262 LSAPDLGIMNCSHPLASFSTACTFICSEGTLLGKKKTIKCSGSIWNSPPTCQKLDK 321
DB 844 LSAPDLGIMNCSHPLASFSTACTFICSEGTLLGKKKTIKCSGSIWNSPPTCQKLDK 903
QY 322 SFSMIKEGDYNLFIPVAVMTAFSGLAFTIILARLKKKKSKR 366
DB 904 SFSMIKEGDYNLFIPVAVMTAFSGLAFTIILARLKKKKSKR 948

RESULT 8

US-60-207-315-428
Sequence 428, Application US/60207315

GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
FILE REFERENCE: C1000601
CURRENT APPLICATION NUMBER: US/60/207,315
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 528
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 428
LENGTH: 1078
TYPE: PRT
ORGANISM: HUMAN
US-60-207-315-428

Query Match 88.8%; Score 1879; DB 23; Length 1078;
Best Local Similarity 97.1%; Pred. No. 1,7e-155;

Matches 335; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 22 GWTMLCCDFLAHHGTYCWTYHYSEKPMNQRRARFCRDNTDVAIQNKAEIYLEKTL 81
DB 604 GYFLPSKDFLAHHGTYCWTYHYSEKPMNQRRARFCRDNTDVAIQNKAEIYLEKTL 663
QY 82 FSRSYWIGIRKIGIMTWGINKSLTEBAENMGDEPNKKKNEKDCVEIYKRNKDGK 141
DB 664 FSRSYWIGIRKIGIMTWGINKSLTEBAENMGDEPNKKKNEKDCVEIYKRNKDGK 723
QY 142 WNDACHKRLKALCYTASCPMWSGSGHGCVEIINNHTCNDGVYGPQOLVIOCEPLE 201
DB 724 WNDACHKRLKALCYTASCPMWSGSGHGCVEIINNHTCNDGVYGPQOLVIOCEPLE 783
QY 202 APELGTMDCTHPGNFSFSSQCAFSCSEGTNLGIEETTCGPRGMSPEPTCOVIOCEP 261
DB 784 APELGTMDCTHPGNFSFSSQCAFSCSEGTNLGIEETTCGPRGMSPEPTCOVIOCEP 843
QY 262 LSAPDLGIMNCSHPLASFSTACTFICSEGTLLGKKKTIKCSGSIWNSPPTCQKLDK 321
DB 844 LSAPDLGIMNCSHPLASFSTACTFICSEGTLLGKKKTIKCSGSIWNSPPTCQKLDK 903
QY 322 SFSMIKEGDYNLFIPVAVMTAFSGLAFTIILARLKKKKSKR 366
DB 904 SFSMIKEGDYNLFIPVAVMTAFSGLAFTIILARLKKKKSKR 948

RESULT 9

US-60-230-435-1751

```

: Sequence 1751, Application US/60230435
: GENERAL INFORMATION:
: APPLICANT: Beasley, Ellen
: TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: C1000768
: CURRENT APPLICATION NUMBER: US/60/230,435
: CURRENT FILING DATE: 2000-09-06
: NUMBER OF SEQ ID NOS: 2991
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1751
: LENGTH: 1078
: TYPE: PRT
: ORGANISM: HUMAN
: US-60-230-435-1751

```

Query Match	88.8%	Score 1879;	DB 23;	Length 1078;
Best Local Similarity	97.1%;	Pred. No. 1.7e+155;		
Matches 335;	Conservative 3;	Mismatches 7;	Indels 0;	Gaps 0

QY	22	GMTWICDDEFLAHSTGYCMTYHSKSPYMMQRRAREPCDNTDLYAIONKAEIYLEKTLR	81
		1 : :	
Db	604	GYFLPSKDFLAHHSTDCDWTTHYSKPKPMQRRAREPCDNTDLYAIONKAEIYLEKTLR	663
QY	82	FSRSYVWIGIRKIGIWTWGTNKSLETEAENMWDGEPNNKKNKEDCEVEIYIKRNKQAG	141
Db	664	FSRSYVWIGIRKIGIWTWGTNKSLETEAENMWDGEPNNKKNKEDCEVEIYIKRNKQAG	723
QY	142	WMDACGKRLAALCYTASCPMWSGSGEGCEVEIINNTCQDVGYYGPOCOLYIOCPLE	201
Db	724	WMDACGKRLAALCYTASCPMWSGSGEGCEVEIINNTCQDVGYYGPOCOLYIOCPLE	783
QY	202	APBLGTMDCHHPGNSBFSSQCAFCSGEBTNLTGIEBTTGPGPNMSSPEPTQVIOCEP	261
Db	784	APBLGTMDCHHPGNSBFSSQCAFCSGEBTNLTGIEBTTGPGPNMSSPEPTQVIOCEP	843
QY	262	LSAPADLGIMNCSHPLASFSTSACTFICSGTELGKKTICSSGIGMSWSPFCQDLK	321
Db	844	LSAPADLGIMNCSHPLASFSTSACTFICSGTELGKKTICSSGIGMSWSPFCQDLK	903
QY	322	SFSMIKRGDYNPLFIPIYAVVWVAFSGIAFLITLARRLKKGKKSKR	366
Db	904	SFSMIKRGDYNPLFIPIYAVVWVAFSGIAFLITLARRLKKGKKSKR	948

RESULT 10
US-09-119-209-4
Sequence 4, Application US/09119209
GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: VEDNOCK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS;
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,209
FILING DATE: 20-Jul-1998

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1 CLASSIFICATION:
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: 08/513278
4 FILING DATE: 10-AUG-1995
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 08/059027
7 FILING DATE: 6-MAY-1993
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: 07/786149
10 FILING DATE: 31-OCT-1991
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: 07/315015
13 FILING DATE: 23-FEB-1989
14 ATTORNEY/AGENT INFORMATION:
15 NAME: Love, Richard B.
16 REGISTRATION NUMBER: 34,659
17 REFERENCE/DOCKET NUMBER: P0565D1C3
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: 650/225-5530
20 TELEFAX: 650/952-9881
21 INFORMATION FOR SEQ ID NO: 4:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 372 amino acids
24 TYPE: Amino Acid
25 TOPOLOGY: Linear
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Query Match	78.0%;	Score 1551;	DB 15;	Length 372;
Best Local Similarity	76.1%;	Pred. No. 4.9e-136;		
Matches 283;	Conservative 32;	Mismatches 57;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 11
PCR-US94-09395-4
; Sequence 4, Application PC/TUS9409395
;
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Oklahoma
; TITLE OF INVENTION: Expression Control Sequences of the P-Selectin Gene
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Patricia L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: GA

```



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; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09395
; FILING DATE: 19-AUG-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 830 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US94-09395-4

Query Match          42.8%; Score 905; DB 1; Length 830;
Best Local Similarity 50.6%; Pred. No. 3,8e-70;
Matches 157; Conservative 47; Mismatches 106; Indels 0; Gaps 0;

QY 8 OSTQDRLMNIETKLMGTMCCDFLAHHGTYCWTYHSEKPMNORARFCRDNYTDLVAI 67
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 11 QRRQVVFVGGISQLCSFALSISLSELTNOEVAMTYHSTKAYSWNISKYQCNRTYDVAI 70
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 68 QNKAEELEYEKTLPFSRSYVWIGIRKIGTWTWVGNKSLTEEAEMNGDEPNKKKKED 127
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 71 QNNNEIDYLNKVLPIYSSTYVWIGIRKNNKTWTWGTAKALTNEAEMNADNEPNKKRNED 130
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 128 CVELIYIKRNDAKWDNDACHKLKALCYTASQPMSCSGHGCEVELINNHTCNDVGY 187
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 131 CVELIYIKSPAPGKWNDEHCKKHALCYTASQDMSCSKGCELETIGNYTCSYCPGFY 190
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 188 GPCCQVLYIOCEPLAEPLGMDCTHPPGNFSFSSQCAFSCSEGTNLTGIEETTCGPGNM 247
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 191 GPCEYVREGCELELPQHVLAMNCSHPLGNFSFNSQCSFHCITDGYQVNGPSKLECLASGIW 250
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 248 SSPEPTCQVIOCEPLASAPDLGIMNCSHPLASFSTSACTFICSEGTLELKKKTTICSSG 307
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 251 TNKPPQCLAAQCPLKIPERGNMICHSAKAFQHOSSCSFCEGFLVGPVYVQCTASG 310
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 308 IWSNPSPIQ 317
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 311 VWTAPAPVCK 320
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
US-08-449-687B-4
; Sequence 4, Application US/08449687B
; GENERAL INFORMATION:
; APPLICANT: McEever, Rodger P.
; APPLICANT: Pan, Junliang
; TITLE OF INVENTION: Expression Control Sequences of the
; TITLE OF INVENTION: P-Selection Gene
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,687B
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/110,158
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA: US 07/320,408
; APPLICATION NUMBER: 08-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)873-8794
; TELEFAX: (404)873-8795
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 830 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-449-687B-4

Query Match          42.8%; Score 905; DB 8; Length 830;
Best Local Similarity 50.6%; Pred. No. 3,8e-70;
Matches 157; Conservative 47; Mismatches 106; Indels 0; Gaps 0;

QY 8 OSTQDRLMNIETKLMGTMCCDFLAHHGTYCWTYHSEKPMNORARFCRDNYTDLVAI 67
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 11 QRRQVVFVGGISQLCSFALSISLSELTNOEVAMTYHSTKAYSWNISKYQCNRTYDVAI 70
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 68 QNKAEELEYEKTLPFSRSYVWIGIRKIGTWTWVGNKSLTEEAEMNGDEPNKKKKED 127
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 71 QNNNEIDYLNKVLPIYSSTYVWIGIRKNNKTWTWGTAKALTNEAEMNADNEPNKKRNED 130
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 128 CVELIYIKRNDAKWDNDACHKLKALCYTASQPMSCSGHGCEVELINNHTCNDVGY 187
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 131 CVELIYIKSPAPGKWNDEHCKKHALCYTASQDMSCSKGCELETIGNYTCSYCPGFY 190
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 188 GPCCQVLYIOCEPLAEPLGMDCTHPPGNFSFSSQCAFSCSEGTNLTGIEETTCGPGNM 247
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 191 GPCEYVREGCELELPQHVLAMNCSHPLGNFSFNSQCSFHCITDGYQVNGPSKLECLASGIW 250
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 248 SSPEPTCQVIOCEPLASAPDLGIMNCSHPLASFSTSACTFICSEGTLELKKKTTICSSG 307
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 251 TNKPPQCLAAQCPLKIPERGNMICHSAKAFQHOSSCSFCEGFLVGPVYVQCTASG 310
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 308 IWSNPSPIQ 317
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 311 VWTAPAPVCK 320
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
US-60-207-315-467
; Sequence 467, Application US/60207315
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO00601
; CURRENT APPLICATION NUMBER: US/60/207,315
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 528
; SOFTWARE: FastSeq for Windows Version 4.0
```

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? SEQ ID NO 467
? LENGTH: 700
? TYPE: PRT
? ORGANISM: HUMAN
? FEATURE:
? NAME/KEY: VARIANT
? LOCATION: (1)..(700)
? OTHER INFORMATION: Xaa = Any Amino Acid
US-60-207-315-467

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Query Match	42.4%	Score 898;	DB 23;	Length 700;
Best Local Similarity	54.1%;	Pred. No. 1.3e-69;		
Matches 151;	Conservative 41;	Mismatches 87;	Indels 0;	Gaps 0

QY	39	WTYHYSEPPMMAQARRPCGRNVDVAIONKKEIETLETPRSRYTWIGJRKIGGIW	98
		: : : : : : : : : : : : : : : : : : : :	
Db	34	WTYHYSTRKASMNISRKYYCCNRTDVAIONKNEIDYLNKVLPRYSSTYWGIRKNNKTW	93
QY	99	TWVGTSKSLTEAEANWGDGEPPNNKRNKEDCEVEIYIKRNKDGKWNDDACHKLAALCYTA	158
		: : : : : : : : : : : : : : : : : : : :	
Db	94	TWVGTSKSLTEAEANWADNEPPNNRNKEDCEVEIYIKSPASPGKWNDDCHCKLRKHALCYTA	153
QY	159	SCQPMSCSGGEGCEVEIINNHNHCNDVDVYVYPOCOLVIOCEPLAPELGTMDCHHPGNGFS	218
		: : : : : : : : : : : : : : : : : : : :	
Db	154	SCQPMSCSGKQCECELETIGNTCSTYPCGFYGECEYVAGECELETPHVLNANCSPHIGNFS	213
QY	219	FSSQCAEFCSEBGTULNIGIEETTCGPFQNMSSPBEPTQVIOICEPLSAADLIMNCSPHLAS	278
		: : : : : : : : : : : : : : : : : : : :	
Db	214	FNSQCFHCTDGYQVNGPSPKIECLASIGITWNNKPPQCLAAQCPPLKPIREGRNMTCLSASKA	273
QY	279	FSTSTACTPICSCEETELIGKKKTIICSSSAGTMSNPSPICQ	317
		: : : : : : : : : : : : : : : : : : : :	
Db	274	FQHOSSCSFSCSEBGFALVGEVQVCAASGAWTLAPAPVCK	312

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RESULT 14
PCT-US99-28965-19
; Sequence 19, Application PC/TUS9928965
; GENERAL INFORMATION:
; APPLICANT: Monla, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION
; FILE REFERENCE: ISFH-0424
; CURRENT APPLICATION NUMBER: PCT/US99/28965
; CURRENT FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: US 9/209,668
; EARLIER FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 610
; TYPE: PR1
; ORGANISM: Homo sapiens
; PCT-US99-28965-19

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Query Match	40.7%;	Score 862;	DB 1;	Length 610;
Best Local Similarity	52.0%;	Pred. No. 1.6e-66;		
Matches 145;	Conservative 41;	Mismatches 93;	Indels 0;	Gaps 0

[illegible]

Db 142 ACTNNSGSHGECVETINNNYCKDKDPGFSGLKCBQIVNCTALSPESRHSGLYVCSHPGLGNS 201

Qy 219 FSSOCAPFCSGSGNTLGTLEETTCGPFQWMSPEPTCOYICEPTASADLIGMNCNSHLAS 278

Db 202 YNSSCSITSCDMDGLYLPSSMETNOCSSGEMSNAPIPACVNYEDDAVTNANGFVECFQNGS 261

Qy 279 FSPISACFFICSEGTGLIGKKKTCESGIMSNSPICO 317

Db 262 FPMWNTCTFFDCSEGFELMGASLOCTSSGMDNKNPKPK 300

RESULT 15
US-08-657-753-2
; Sequence 2, Application US/08657753
CURRENT INNOVATION:

APPLICANT: Klimuk, Sandra K.
 APPLICANT: Semple, Sean C.
 APPLICANT: Scherrer, Peter
 APPLICANT: Hope, Michael J.
 TITLE OF INVENTION: Enhanced Efficacy of Liposomal Antisense
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/657,753
 FILING DATE: Not yet assigned
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Kezer, William B.
 REGISTRATION NUMBER: 37,369
 REFERENCE/DOCKET NUMBER: 16303-003600
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 610 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match	40.7%;	Score 862;	DB 10;	Length 610;
Best Local Similarity	52.0%;	Pred. No. 1.6e-66;		
Matches 145;	Conservative 41;	Mismatches 93;	Indels 0;	Gaps 0;

[illegible]

OY 279 FSPYSACTFICSEGTLELIGKKRTICESSGIWSNPICQ 317
| : : ||| | ||| : | ||| | | :
Db 262 FPMWTCTCTFDOEBEGFELMGAQSLQCTSSGNMNDNEKPTCK 300

Search completed: October 13, 2001, 02:58:37
Job time: 593 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 13, 2001, 02:54:07 ; Search time 52.07 Seconds

(without alignments)
355.184 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116

Sequence: 1 MIFPMKQSTQORDLNMIFKLMGWTMLCCDFLAHHGTYCWTYHSEKPMNORARFCRDN 372

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 329605 seqs, 49716248 residues

Total number of hits satisfying chosen parameters: 329605

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending patents, AA, New: *
1: /cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgnl_7/ptodata/2/paa/US01-26675-3
3: /cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgnl_7/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgnl_7/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2094	99.0	382	5	US-09-760-475-2123
2	2090	98.8	372	1	PCT-US01-26675-3
3	1807	85.4	341	5	US-09-758-449-1158
4	1807	85.4	341	5	US-09-760-443-1328
5	999	47.2	184	5	US-09-760-443-1437
6	999	47.2	184	5	US-09-760-475-3252
7	862	40.7	610	5	US-09-784-356-122
8	473	22.4	196	5	US-09-760-498-916
9	283.5	13.4	355	5	US-09-764-902-1145
10	274.5	13.0	208	5	US-09-760-473-2126
11	270	12.8	207	5	US-09-760-443-1321
12	270	12.8	207	5	US-09-760-498-920
13	270	12.8	207	5	US-09-760-475-3255
14	266	12.6	309	5	US-09-764-875-615
15	246.5	11.6	3571	5	US-09-911-842-2
16	239	11.3	3594	5	US-09-911-842-4
17	222	10.5	138	5	US-09-764-875-938
18	222	10.5	138	5	US-09-764-902-1688
19	183	8.6	326	5	US-09-787-192-11
20	183	8.6	328	5	US-09-787-192-2
21	183	8.6	333	5	US-09-764-870-279
22	172	8.1	1929	1	PCT-US01-08631-30462
23	172	8.1	2039	1	PCT-US01-08631-30466
24	172	8.1	2489	5	US-09-911-842-5
25	170	8.0	404	5	US-09-891-894-1
26	170	8.0	404	6	US-60-300-971-1
27	168	7.9	1139	5	US-09-764-893-102

28	168	7.9	1139	5	US-09-764-853-634	Sequence 634, App
29	168	7.9	1139	5	US-09-764-875-873	Sequence 873, App
30	168	7.9	1139	5	US-09-764-881-99	Sequence 99, App1
31	168	7.9	1139	5	US-09-764-898-204	Sequence 204, App1
32	166	7.8	1184	1	PCT-US01-08631-51085	Sequence 51085, A
33	165.5	7.8	1479	5	US-09-918-715-305	Sequence 305, App
34	164	7.8	330	5	US-09-545-551A-14	Sequence 14, App1
35	162	7.7	1722	5	US-09-194-612A-1	Sequence 1, App1
36	162	7.7	1740	1	PCT-US01-08631-553205	Sequence 53205, A
37	161	7.6	1479	5	US-09-918-715-238	Sequence 238, App
38	160	7.6	130	5	US-09-760-443-870	Sequence 870, App
39	158.5	7.5	470	5	US-09-760-475-2121	Sequence 2121, App
40	158	7.5	497	5	US-09-764-893-125	Sequence 125, App
41	158	7.5	487	5	US-09-764-853-816	Sequence 816, App
42	158	7.5	487	5	US-09-764-875-1154	Sequence 1154, App
43	158	7.5	497	5	US-09-764-881-157	Sequence 157, App
44	158	7.5	497	5	US-09-764-898-276	Sequence 276, App
45	156.5	7.4	1627	1	PCT-US01-08656-9868	Sequence 9868, App

ALIGNMENTS

RESULT 1
US-09-760-475-2123
; Sequence 2123, Application US/09760475
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT249
; CURRENT APPLICATION NUMBER: US/09/760,475
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 4122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2123
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-760-475-2123

Query Match	99.0%	Score 2094;	DB 5;	Length 382;
Best Local Similarity	99.2%	Pred. No. 1.6e-169;		
Matches 369;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
OY	1	MIFPMKQSTQORDLNMIFKLMGWTMLCCDFLAHHGTYCWTYHSEKPMNORARFCRDN	60	
DB	11	MIFPMKQSTQORDLNMIFKLMGWTMLCCDFLAHHGTYCWTYHSEKPMNORARFCRDN	70	
OY	61	YTDLVAIONKAEIYELEKTLPEFSRSYWIIGIRKIGIMTVGINKSLTEAEENMGDEPN	120	
DB	71	YTDLVAIONKAEIYELEKTLPEFSRSYWIIGIRKIGIMTVGINKSLTEAEENMGDEPN	130	
OY	121	NKKRKECEVETIYIKRNDADKAMDACHIKALKALCYASQPMSCSHGCEVELINNHTC	180	
DB	131	NKKRKECEVETIYIKRNDADKAMDACHIKALKALCYASQPMSCSHGCEVELINNHTC	190	
OY	181	NCDEVGYGPCOLVIOCEPLEAPELGTMCTHPGNSFSFSCAFSCSEGTNLGIEETT	240	
DB	191	NCDEVGYGPCOLVIOCEPLEAPELGTMCTHPGNSFSFSCAFSCSEGTNLGIEETT	250	
OY	241	CGPFGNMSSEPTCQVIOCEPLASPDGIMNCSHPLASFSTACTPFCSEGTLLIKKK	300	
DB	251	CGPFGNMSSEPTCQVIOCEPLASPDGIMNCSHPLASFSTACTPFCSEGTLLIKKK	310	
OY	301	TICSSGSIWNSPSTICKLKDSFSMIKEGYNPLFTVAVWVAFAFSLATIMLARBKK	360	
DB	311	TICSSGSIWNSPSTICKLKDSFSMIKEGYNPLFTVAVWVAFAFSLATIMLARBKK	370	
OY	361	GKSKSRSMNDPY 372		
DB	371	GKSKSRSMNDPY 382		

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RESULT 2
PCT-US01-26675-3
; Sequence 3, Application PC/TUS0126675
; GENERAL INFORMATION:
; APPLICANT: Genassance Pharmaceuticals, Inc.
; APPLICANT: Anastasio, Allison E
; APPLICANT: Bieglecki, Katryn M
; APPLICANT: Klem, Stefanie E
; APPLICANT: Koshiy, Beena
; APPLICANT: Kumar, Anant Madan
; TITLE OF INVENTION: HAPLOTYPES OF THE SELL GENE
; FILE REFERENCE: SELL MWH1116-PCT
; CURRENT APPLICATION NUMBER: PCT/US01/26675
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 60/228,262
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 3
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-26675-3

Query Match          98.8%; Score 2090; DB 1; Length 372;
Best Local Similarity 98.9%; Pred. No. 3.5e-169;
Matches 368; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIFPMKOSTORDLNIIFKMGWTMLCCDFLAHGGTYCWTYHSEKPMNORARRCRDN 60
DB 1 MIFPMKOSTORDLNIIFKMGWTMLCCDFLAHGGTYCWTYHSEKPMNORARRCRDN 60
QY 61 YTDLVAIQKAEIYELEKTLPPRSRYTWIGIRKIGIWTWGTNKSLTBEAENWGDEPN 120
DB 61 YTDLVAIQKAEIYELEKTLPPRSRYTWIGIRKIGIWTWGTNKSLTBEAENWGDEPN 120
QY 121 NKKNKEDCEIYIKRKNDGKNNDDACHLKAALCTTASCQWPSGSGHGECEIINNHTC 180
DB 121 NKKNKEDCEIYIKRKNDGKNNDDACHLKAALCTTASCQWPSGSGHGECEIINNHTC 180
QY 181 NCDVGYGPOCOLVIOCEPLEAELGTMDCTHPFGNFSFSSOCARFSCSGTNLGIEETT 240
DB 181 NCDVGYGPOCOLVIOCEPLEAELGTMDCTHPFGNFSFSSOCARFSCSGTNLGIEETT 240
QY 241 CGPFGMWSSPEPTCOYIOCEPLSAPDLGIMNCSHPLASFSTSACTFICSEGTELIGKKK 300
DB 241 CGPFGMWSSPEPTCOYIOCEPLSAPDLGIMNCSHPLASFSTSACTFICSEGTELIGKKK 300
QY 301 TICSESGIMSNSPICQIKDKSFSMTKEGDYNPLFPVAVMTAFSGLAFTIWLARLKK 360
DB 301 TICSESGIMSNSPICQIKDKSFSMTKEGDYNPLFPVAVMTAFSGLAFTIWLARLKK 360
QY 361 GKSKRSMDPY 372
DB 361 GKSKRSMDPY 372

RESULT 3
US-09-758-449-1158
; Sequence 1158, Application US/09758449
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM026
; CURRENT APPLICATION NUMBER: US/09/758,449
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
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; NUMBER OF SEQ ID NOS: 1478
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1158
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (215)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-449-1158

Query Match          85.4%; Score 1807; DB 5; Length 341;
Best Local Similarity 98.7%; Pred. No. 2.9e-145;
Matches 313; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIFPMKOSTORDLNIIFKMGWTMLCCDFLAHGGTYCWTYHSEKPMNORARRCRDN 60
DB 23 MIFPMKOSTORDLNIIFKMGWTMLCCDFLAHGGTYCWTYHSEKPMNORARRCRDN 82
QY 61 YTDLVAIQKAEIYELEKTLPPRSRYTWIGIRKIGIWTWGTNKSLTBEAENWGDEPN 120
DB 83 YTDLVAIQKAEIYELEKTLPPRSRYTWIGIRKIGIWTWGTNKSLTBEAENWGDEPN 142
QY 121 NKKNKEDCEIYIKRKNDGKNNDDACHLKAALCTTASCQWPSGSGHGECEIINNHTC 180
DB 143 NKKNKEDCEIYIKRKNDGKNNDDACHLKAALCTTASCQWPSGSGHGECEIINNHTC 202
QY 181 NCDVGYGPOCOLVIOCEPLEAELGTMDCTHPFGNFSFSSOCARFSCSGTNLGIEETT 240
DB 203 NCDVGYGPOCOLVIOCEPLEAELGTMDCTHPFGNFSFSSOCARFSCSGTNLGIEETT 262
QY 241 CGPFGMWSSPEPTCOYIOCEPLSAPDLGIMNCSHPLASFSTSACTFICSEGTELIGKKK 300
DB 263 CGPFGMWSSPEPTCOYIOCEPLSAPDLGIMNCSHPLASFSTSACTFICSEGTELIGKKK 322
QY 301 TICSESGIMSNSPICQ 317
DB 323 TICSESGIMSNSPICQ 339

RESULT 4
US-09-760-443-1328
; Sequence 1328, Application US/09760443
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ212
; CURRENT APPLICATION NUMBER: US/09/760,443
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2164
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1328
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (215)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-443-1328

Query Match          85.4%; Score 1807; DB 5; Length 341;
Best Local Similarity 98.7%; Pred. No. 2.9e-145;
Matches 313; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIFPMKOSTORDLNIIFKMGWTMLCCDFLAHGGTYCWTYHSEKPMNORARRCRDN 60
DB 23 MIFPMKOSTORDLNIIFKMGWTMLCCDFLAHGGTYCWTYHSEKPMNORARRCRDN 82
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QY 61 YTDLVAIONKAEIYLEKTLPEFSRSYYWIGIRKIGIWTWGTNKSITJEEAENMGDEPN 120
      |||
      |||
      |||
Db 83 YTDLVAIONKAEIYLEKTLPEFSRSYYWIGIRKIGIWTWGTNKSITJEEAENMGDEPN 142
      |||
      |||
      |||
QY 121 NKKNKEDCYEIIYIKRKKDAGKWDACCHLKALCTTASQPMSCSGHGCVELINNHTC 160
      |||
      |||
      |||
Db 143 NKKNKEDCYEIIYIKRKKDAGKWDACCHLKALCTTASQPMSCSGHGCVELINNHTC 202
      |||
      |||
      |||
QY 181 NCDVGYGPOCOVIOCEPLAPDLGIMNCSPHPLASFSTACTFICSEGTNLGIEETT 240
      |||
      |||
      |||
Db 203 NCDVGYGPOCOVIOCEPLAPDLGIMNCSPHPLASFSTACTFICSEGTNLGIEETT 262
      |||
      |||
      |||
QY 241 CGPFGNMSPEPTCOVIOCEPLAPDLGIMNCSPHPLASFSTACTFICSEGTNLGIEETT 300
      |||
      |||
      |||
Db 263 CGPFGNMSPEPTCOVIOCEPLAPDLGIMNCSPHPLASFSTACTFICSEGTNLGIEETT 322
      |||
      |||
      |||
QY 301 TICSSGIMNSPICO 317
      |||
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Db 323 TICSSGIMNSPICO 339
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RESULT 5
US-09-760-443-1437
; Sequence 1437, Application US/09760443
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P212
; CURRENT APPLICATION NUMBER: US/09/760,443
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2164
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1437
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-443-1437

Query Match 47.2%; Score 999; DB 5; Length 184;
Best Local Similarity 99.5%; Pred. No. 3.5e-77;
Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 189 PQOLVIOCEPLAPDLGIMNCSPHPLASFSTACTFICSEGTNLGIEETTGPFGNMS 248
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      |||
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Db 1 PQOLVIOCEPLAPDLGIMNCSPHPLASFSTACTFICSEGTNLGIEETTGPFGNMS 60
      |||
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      |||
QY 249 SPEPTCOVIOCEPLAPDLGIMNCSPHPLASFSTACTFICSEGTNLGIEETTGPFGNMS 308
      |||
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Db 61 SPEPTCOVIOCEPLAPDLGIMNCSPHPLASFSTACTFICSEGTNLGIEETTGPFGNMS 120
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QY 309 WSNPSPICOKLDSFSMIKGGDYNPLFIPAVVWTAFFSGLAFITWLARRLKKKKSRSM 368
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Db 121 WSNPSPICOKLDSFSMIKGGDYNPLFIPAVVWTAFFSGLAFITWLARRLKKKKSRSM 180
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QY 369 NDPY 372
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Db 181 NDPY 184
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      |||
      |||

RESULT 6
US-09-760-475-3252
; Sequence 3252, Application US/09760475
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT249
; CURRENT APPLICATION NUMBER: US/09/760,475
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4122
; SOFTWARE: Patentln Ver. 2.0
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; SEQ ID NO 3252
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-475-3252

Query Match 47.2%; Score 999; DB 5; Length 184;
Best Local Similarity 99.5%; Pred. No. 3.5e-77;
Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 189 PQOLVIOCEPLAPDLGIMNCSPHPLASFSTACTFICSEGTNLGIEETTGPFGNMS 248
      |||
      |||
      |||
Db 1 PQOLVIOCEPLAPDLGIMNCSPHPLASFSTACTFICSEGTNLGIEETTGPFGNMS 60
      |||
      |||
      |||
QY 249 SPEPTCOVIOCEPLAPDLGIMNCSPHPLASFSTACTFICSEGTNLGIEETTGPFGNMS 308
      |||
      |||
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Db 61 SPEPTCOVIOCEPLAPDLGIMNCSPHPLASFSTACTFICSEGTNLGIEETTGPFGNMS 120
      |||
      |||
      |||
QY 309 WSNPSPICOKLDSFSMIKGGDYNPLFIPAVVWTAFFSGLAFITWLARRLKKKKSRSM 368
      |||
      |||
      |||
Db 121 WSNPSPICOKLDSFSMIKGGDYNPLFIPAVVWTAFFSGLAFITWLARRLKKKKSRSM 180
      |||
      |||
      |||
QY 369 NDPY 372
      |||
      |||
      |||
Db 181 NDPY 184
      |||
      |||
      |||

RESULT 7
US-09-784-356-122
; Sequence 122, Application US/09784356
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: EOS Biotechnology, Inc.
; TITLE OF INVENTION: Novel Methods of Diagnosis of Angiogenesis,
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
; TITLE OF INVENTION: Modulators
; FILE REFERENCE: 018501-000710US
; CURRENT APPLICATION NUMBER: US/09/784,356
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 60/148,425
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 09/637,977
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 122
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-784-356-122

Query Match 40.7%; Score 862; DB 5; Length 610;
Best Local Similarity 52.0%; Pred. No. 5.9e-65;
Matches 145; Conservative 41; Mismatches 93; Indels 0; Gaps 0;

QY 39 WTYHYSEKPMNMOARARFCRDNYTDLVAIONKAEIYLEKTLPEFSRSYYWIGIRKIGI 98
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      |||
Db 22 WSYNTSTREANTYDEASAYCQORHTHLVAIONKEIEYELNSILSPSYWIGIRKANVNW 81
      |||
      |||
      |||
QY 99 TWGTNKSITJEEAENMGDEPNKKKKEDCEVEIYIKRKKDAGKWDACCHLKALCTTAS 158
      |||
      |||
      |||
Db 82 VWVGTOKPLTEBAKNWAPGEPNNRQKDEDCVEIYIKRKKDAGKWDACCHLKALCTTAS 141
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QY 159 SCOPWSCSGHGECEIINNHTCNDVGYGPOCOVIOCEPLAPDLGIMNCSPHPLASF 218
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      |||
      |||
Db 142 ACTNWTSCSGHGECEIINNHTCNDVGYGPOCOVIOCEPLAPDLGIMNCSPHPLASF 201
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      |||
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QY 219 FSSQAFSCSEGTNLGIEETTGPFGNMSPEPTCOVIOCEPLAPDLGIMNCSPHPLASF 278
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Db	16	PTCE-AVNCDAVHQPRKGLVRCANSPIGEFIFYKSCAFSCSEEGELHSGTQLECTSQGQM	74
QY	248	SSPEPTCOVICDEPLSAPADUGIMNCS-HPLASESFSTACTFFICSEGTIELIGKKTTICESS	306
		: :	
Db	75	TEEVPSQCQVVKCSSLAVPBGKINMSCSEBPV---FGTVCKFACPEGMTLNGSAARTGAT	130
QY	307	GIMSNPSTICQLDKDSFSMKIEGGIYNFLT-----PAVANVTAFSGLAFTIWLARKLKKG	361
		: :	
Db	131	GHWSGLLPFCRAKYTE--SNIPLGSMTELXLDXSXGPLA-----PFLTLWRKSLSRKA	179
QY	362	KK 363	
		:	
Db	180	KB 181	

```

RESULT 11
US-09-760-443-1321
: Sequence 1321, Application US/09760443
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PJ212
: CURRENT APPLICATION NUMBER: US/09/760,443
: PRIORITY FILING DATE: 2001-01-16
: Prior application data removed - refer to PALM or file wrapper
: NUMBER OF SEQ ID NOS: 2164
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1321
: LENGTH: 207
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (151)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (185)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (191)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (194)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (198)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: US-09-760-443-1321

```

Query Match	12.8%;	Score 270;	DB 5;	Length 207;
Best Local Similarity	31.6%;	Pred. No. 2.1e-15;		
Matches 60;	Conservative 26;	Mismatches 64;	Indels 40;	Gaps 7;

[illegible]

RESULT 12
US-09-760-498-920

```

: Sequence 920, Application US/09760498
:
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC017
: CURRENT APPLICATION NUMBER: US/09/760,498
: CURRENT FILING DATE: 2001-01-16
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 930
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 920
:
: LENGTH: 207
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: SITE
: LOCATION: (151)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
:
: NAME/KEY: SITE
: LOCATION: (185)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
:
: NAME/KEY: SITE
: LOCATION: (191)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
:
: NAME/KEY: SITE
: LOCATION: (194)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
:
: NAME/KEY: SITE
: LOCATION: (198)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
:
: OS-09-760-498-920

```

Query Match	12.8%;	Score 270;	DB 5;	Length 207;
Best Local Similarity	31.6%;	Pred. No. 2.1e-15;		
Matches 60;	Conservative 26;	Mismatches 64;	Indels 40;	Gaps 7

```

OY 189 POCOLVIOCEPLAEPLGTMCTH-PRGNFESSQCAFSCSEGNLIGIEBTTCGPNGN 247
    18  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 16 PTCE-AVGCDAVHQPCKGLVACASPIGIEFTYKSCAFSCBEGELNGSTQLECTSOGN 74
    16  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 248 SSPEPTCOVIOCEPLASBDIGIMNCS-HPLASFSTACTFICSEGTELIGKKITCESS 306
    24  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 75 TEEVSCQVAKCSSLAIVGKIMNCSGCBPV---FGIVCKFACEDEGWTLNGSAARTGAT 130
    75  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 307 GIMNSPSTICQKLDKSFMSIKEGDTNPLT-----PVAVMTAFSGLAFTW 353
    30  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 GHWSSLTPTC-----EVLSPFTIGLDFSCMDSSSGPLA-----PFLTW 170
    13  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 354 LARRLKKGK 363
    35  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 171 LRKSLRKAKK 180
    17  : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 13
US-09-760-475-3255
: Sequence 3255, Application US/09760475
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PT49
: CURRENT APPLICATION NUMBER: 09/09/760,475
: CURRENT FILING DATE: 2001-01-16
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 4122
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3255
: LENGTH: 207
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (151)

```

```
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (185)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (191)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (194)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (198)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-760-475-3255
```

```
Query Match          12.8%; Score 270; DB 5; Length 207;
Best Local Similarity 31.6%; Pred. No. 2.1e-15;
Matches 60; Conservative 26; Mismatches 64; Indels 40; Gaps 7;
```

```
OY 189 POCQVIOCEPLEAPDLGTMDCDH-PFGNFSFSSQCAFSCSEGTNLGIEETTCGPGNWSPEPTC 247
DB 16 PTCE-AVRCDAAHOPPKGLVRCASHPIGEFTYKSSCAFCSEGEFELHGSTOLECTSOQGM 74
OY 248 SSEPTECOVIOCEPLSAPDLGIMNCS-HPLASFSTACTICSEGTTELIGKKTTICESS 306
DB 75 TEVVSQVYKCSSLAIPKIMKSCGEPV-----PCTVCKFACPEBMTLNGSAARCTCAT 130
OY 307 GIMNSPICOQLDKSFSMIKEDYNPLFI-----PVAVMVTAFSGLAFITM 353
DB 131 GIMSGILPFC-----EVLSPPTLGLKDFSCMDSSGSLA-----PFLIM 170
OY 354 LARRLKKGK 363
DB 171 LRKSLRKAKK 180
```

```
RESULT 14
US-09-764-875-615
; Sequence 615, Application US/09764875
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1202
; CURRENT APPLICATION NUMBER: US/09/764,875
; PRIOR APPLICATION DATA REMOVED - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 615
; LENGTH: 309
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-764-875-615
```

```
Query Match          12.6%; Score 266; DB 5; Length 309;
Best Local Similarity 31.5%; Pred. No. 7.6e-15;
Matches 58; Conservative 23; Mismatches 81; Indels 22; Gaps 2;
```

```
OY 195 IOCEPLEAPDLGTMDCDH-PFGNFSFSSQCAFSCSEGTNLGIEETTCGPGNWSPEPTC 254
DB 119 VCCPALTTGGGCGCRHHPGTGFTTCYFCGNAGFTLIGDSTLCRPSGQWTAVTPAC 178
OY 255 QVIOCEPLSAPDLGIMNCSHPLASFSTACTICSEGTTELIGKKTTICESSGIMNSPSP 314
DB 179 RAVKCESELVNNPIRANCSNLMGNFSYGISCFHCLGQLNLSAQTAQDENHMTYVP 238
OY 315 ICOKLDRSFSMIKEDYNPLFI-----PVAVMVTAFSGLAFITMILARRLKKGKSK 365
DB 239 TCGA-----GFLTIOEALTYFGANVASTIGLIMGTLLALLRKRRROKDDK 285
OY 366 RSMN 369
```

```
DB 286 CPLN 289
```

```
RESULT 15
US-09-911-842-2
; Sequence 2, Application US/09911842
; GENERAL INFORMATION:
; APPLICANT: Welcher, Andrew A.
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37592
; CURRENT APPLICATION NUMBER: US/09/911,842
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 60/222,438
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 3571
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-911-842-2
```

```
Query Match          11.6%; Score 246.5; DB 5; Length 3571;
Best Local Similarity 28.9%; Pred. No. 6.4e-12;
Matches 63; Conservative 33; Mismatches 93; Indels 29; Gaps 8;
```

```
OY 138 DAGKMWDACHKIKALCYTASCQPMSCSGHGECEVITINNHTCNCDVGY--GPOCQVLY 195
DB 1732 DNGSMNVGPSCLDVDECAVGS---DCSEHASCINLVDSYSICVPPYTGDKNCAEPI 1787
OY 196 OCEPLEAPDLGTMDCDHPPGN--FSFSSQCAFSCSEGTNLGIEETTCGPGNWSPEPTC 254
DB 1788 KCKAPGNPENG-----HSGEITYGAELVTFSCQEGYQLMGVYKTKTCLSGERNHLIPYC 1842
OY 255 QVIOCEPLSAPDLGIMNCSHPLASFSTACTICSEGTTELIGKKTTICESSGIMNSPSP 314
DB 1843 KAVSCGKPAIPENG---CIEELA-FTFGSKVYTRCKKGYTLADGKESCLANSWSHSP 1898
OY 315 ICOKLD-KSFSMIKEDYNPLFI-PVAVMVTAFSGLAFI 351
DB 1899 VCEPVKSSPENINNGKY-----ILSGLYL 1924
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Search completed: October 13, 2001, 03:00:39
Job time: 392 sec
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